DEGI AVAILABLE CON

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

April 21, 2005, 04:17:43; Search time 219.5 Seconds (without alignments) 1185.131 Million cell updates/sec

US-09-016-159D-5
2715
1 MDHLGASLWPQVGSLCLLLA......YENSLIPAABPLPPSYVACS 508

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P19235 homo sapien	ans a	P14753 mus musculu	Q07303 rattus norv	Q95nl3 ovis aries	Q95n14 ovis aries	035545 rattus norv	Q27950 bos indicus	Q28206 bos taurus	Q6uap7 tetraodon n				Q6jta8 sus scrofa	Q28235 cervus elap	Q08351 mus musculu	Q28172 bos taurus	Q8brx0 mus musculu	Q6uan4 tetraodon n	Q9hbe5 homo sapien	homo	homo	บรณ	P14787 oryctolagus	Q6nsj8 homo sapien	P32927 homo sapien	Q8c2g1 mus musculu	Q63216 rattus norv	_	Q01114 mus musculu	Q6uam6 tetraodon n
SUMMARIES	ID	EPOR HUMAN	EPOR PIG	EPOR_MOUSE	EPOR RAT	Q95N <u>1</u> 3	Q95N14	035545	Q27950	Q28206	Q6UAP7	IL9R_HUMAN	QGIYE8	Q925F5	PRLR_PIG	PRLR_CEREL	TPOR_MOUSE	PRLR BOVIN	QBBRXO	Q6UAN4	I21R_HUMAN	QGICEO	TPOR_HUMAN	I21R_MOUSE	PRLR_RABIT	Q6NSJ8	CYRB_HUMAN	Q8C2G1	063216	PRLR_SHEEP	IL9R_MOUSE	Q6UAM6
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de	Query Match	100.0	84.1	0	σ	~	0	39.0	~	37.2	•	9.5	8.5	8.3		8.0	8.0	7.9	7.9	7.9	7.8	7.8	7.8	7.7	7.7	7.7	7.7	7.6	7.6	7.5	7.4	7.4
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195.5 192.5 191.5 191.5 189.5 186.5 184.5 183.5 183.5 183.5

ALIGNMENTS

us-09-016-159d-5.rup

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LIGAND BINDING SITE, AND MUTAGENESIS OF THR-114; SER-115; SER-116;
PHE-117; VAL-118; LEU-120; GLU-121; ARG-165; MET-174; SER-176; HIS-177
AND ARG-179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8662939; DOI=10.1074/jbc.271.24.14045; Middleton S.A., Johnson D.L., Jin R., McMahon F.J., Collins A., Tullai J., Gruninger R.H., Jolliffe L.K., Mulcahy L.S.; Identification of a critical ligand binding determinant of the human erythropoietin receptor. Evidence for common ligand binding motifs in the cytokine receptor family.";
                                                                                                                                                                                                                                      TISSUE-Erythroid cells;
MEDLINE-92039091; PubMed=1657727; DOI=10.1016/0378-1119(91)90213-U;
Todokoro K., Kuramochi S., Nagasawa T., Abe T., Ikawa Y.;
"Isolation of a cDNA encoding a potential soluble receptor for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATI/STAT3 ACTIVATION, AND MUTAGENESIS OF TYR-456 AND TYR-468.
PubMed=11756159; DOI=10.1182/blood.V99.1.102;
Kirito K., Nakajima K., Watanabe T., Uchida M., Tanaka M., Ozawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of the human erythropoietin receptor region required for Statl and Stat3 activation."; slood 99:102-110(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12746455; DOI=10.1074/jbc.M210039200; Friedman A.D., Nimbalkar D., Quelle F.W.; "Erythropoietin receptors associate with a ubiquitin ligase, p33RUL, and require its activity for erythropoietin-induced proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "APS, an adaptor protein containing Pleckstrin homology (PH) and Src homology-2 (SH2) domains inhibits the JAK-STAT pathway in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99301417; PubMed-10374881; Metsup M., Inoue A., Komiya S., Wakioka T., Sasaki A., Mitsui K., Yokouchi M., Inoue A., Komiya S.,
                                                                 Penny L.A., Forget B.G.; "Genomic organization of the human erythropoietin receptor gene."; Genomics 11:974-980(1991).
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Tauchi T., Peng G.-S., Shen R., Hoatlin M., Bagby G.C. Jr., Kabat
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"Involvement of SH2-containing phosphotyrosine phosphatase Syp in erythropoietin receptor signal transduction pathways.";
J. Biol. Chem. 270:5631-5635(1995).
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"Increased cell surface expression of C-terminal truncated erythoropoietin receptors in polycythemia.";
Eur. J. Haematol. 67:88-93(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 271:14045-14054(1996).
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                                                                                                                                                                                                            SEQUENCE FROM N.A. (EPOR-S)
SEQUENCE OF 1-17 FROM N.A.
MEDLINE=92147143; PubMed=1664413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukemia 13:760-767(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 106:283-284(1991).
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Ad la Chappelle A., Traskelin A.-L., Juvonen E.;

Ad la Chappelle A., Traskelin A.-L., Juvonen E.;

Truncated erythropietin receptor causes dominantly inherited benign

Truncated erythropoietin receptor causes dominantly inherited benign

E. Droc. Natl. Acad. Sci. U.S.A. 90:4455-4499(1993)

C. I. FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-

C. Induced erythroblast proliferation and differentiation. Upon EPO

C. Induced erythroblast proliferation and differentiation. Upon EPO

C. I. FUNCTION: Receptor EPOR timesing the JAK2/STAT5 signaling

C. I. FUNCTION: Isoform EPOR-T, missing the cytoplasmic tail, acts as a

dominant-negative receptor of EPOR-mediated signaling.

C. I. FUNCTION: Isoform EPOR-T, missing the cytoplasmic tail, acts as a

dominant-negative receptor of EPOR-mediated signaling.

C. SUBUNIT: Forms homodimers on EPO stimulation. The tyrosine-

phosphorylacted form interacts with several SH2 domain-containing

proteins including LYN (By similarity), the adapter protein APS,

C. FYA-45 and inhibits signaling through the DAK-STAT signaling.

C. Shading to PPIPUL, preferentially through the N-terminal SH2

C. Shading to PPIPUL, preferentially through the N-terminal SH2

C. Shading to PPIPUL, preferentially through the N-terminal SH2

C. Shading to PPIPUL, preferentially through the N-terminal SH2

C. Shading to PPIPUL, preferential and phosphorylation of PIPULL

C. Call-warface expression (By similarity). Interaction of PIPULL

C. Call-warface expression (By similarity). Interaction of Coll-warface.

C. Call-warface expression (By similarity).
                                                                                                                                                                     X-TAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
MEDLINE=96291992; PubMed=8662530;
Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,
Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;
"Functional mimicry of a protein hormone by a peptide agonist: the EPO receptor complex at 2.8 A.";
Science 273:464-471(1996).
                                                                         Cloning and characterization of a family of proteins associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein. Isoform EPOR-S is secreted and located to the cell surface.
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"Efficiency of signalling through cytokine receptors depends critically on receptor orientation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.40 ANGSTROMS) OF 34-246.
MEDLINE=99141272; PubMed=9974392; DOI=10.1126/science.283.5404.987;
Livnah O., Stura E.A., Middleton S.A., Johnson D.L., Jolliffe L.K.,
Wilson I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitin ligame NOSIP mediates EPO-induced cell proliferation. Interaction with the Interaction with ATYNOI
                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
MEDLINE=99023198; PubMed=9808045;
MIDLINE=90023198; PubMed=9808045;
MEDLINE=90023198; PubMed=9808045;
You You Johnson D.L. Stura E.A., Farrell F.X., Barbone F.P., You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S., Jolliffe L.K., Wilson I.A.;
An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation.";
Nat. Struct. Biol. 5:993-1004(1998).
                        Meunier C.F., Bordereaux D., Porteu F., Gisselbrecht S., Chretien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystallographic evidence for preformed dimers of erythropoietin receptor before ligand activation."; Science 283:987-990(1999).
MEDLINE=21883980; PubMed=11784712; DOI=10.1074/jbc.M105970200;
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Event=Alternative splicing; Named isoforms=3;
Name=EPOR-F; Synonyms=Full-length form;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVOLVEMENT IN FAMILIAL ERYTHROCYTOSIS.
                                                                                                      Mpl.";
J. Biol. Chem. 277:9139-9147(2002)
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                                                      Courtois G
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activation.
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                                                                                                                                                             ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 180
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                                                                        1 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL
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                                                    Gaps
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Christenson R.K., Vallet J.L.;
"Porcine erythropoietin receptor: molecular cloning and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryonic and fetal liver.",
Domest. Anim. Endocrinol. 19:25-38(2000).
-!- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-
induced erythroblast proliferation and differentiation. Upon EPO stimulation, EPOR dimerizes triggering the JAK2/STATS signaling cascade. In some cell types, can also activate STATI and STATI.
May also activate LYN tyrosine kinase (By similarity).
-!- SUBUNIT: Forms homodimers on EPO stimulation. The tyrosine-
phosphorylated form interacts with several SH2 domain-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                               DB 1; Length 508;
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                                         Pred. No. 4.8e-181;
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29-MAR-2004 (Rel. 43, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Erythropoietin receptor precursor (EPO-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 AA
                                                   0; Mismatches
                               Score 2715;
IsoId=P19235-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SDGPYSNPYENSLIPAAEPLPPSYVACS 508
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          Name=EPOR-S; Synonyms=Soluble form;
                               100.08;
                                          100.08;
                                        Best Local Similarity 100.
Matches 508; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
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Q9MYZ9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
proteins including LYN, the adapter protein APS, PTPN6, PTPN11, JAK2, PI3 kinaese, STATSA/B, SOCS3 and CRKL. The N terminal SH2 domain of PTPN6 binds Tyr-455 and inhibits signaling through dephosphorylation of JAK2. APS binding also inhibits the JAK-STAT signaling. Binding to PTPN11, preferentially through the N-terminal SH2 domain, promoces mitogenesis and phosphorylation of PTPN11. Binding of JAK2 (through its N-terminal) promoces cellsurface expression. Interaction with the ubiquitin ligase NOSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Containing phosphateses.

PTM: On EPO stimulation, phosphorylated on C-terminal tyrosine residues by JAK2. The phosphotyrosine motifs are also recruitment sites for several SH2-containing proteins and adapter proteins which mediate cell proliferation. Phosphorylation on Tyr-455 is required for PTPM interaction, Tyr-427 for PTPM11. Tyr-427 is preferred binding site (By similarity).

PTM: Ubjquitinated by NOSIP; appears to be either multimonoubjquitinated by NOSIP; appears to be either multimonoubjquitinated or polyubjquitinated. Ubjquitation mediates SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                                                                                                                                                                                                                                                                            Bimilarity).

SUBCELLUIAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: Low expression at day 24 gestation in fetal liver. Expression increases dramatically thereafter to day 30. Levels then remain constant up to day 40. Levels then remain constant up to day 40. Levels then remain constant up to be necessary for proper protein folding and thereby efficient intracellular transport and cellsurface receptor binding.

DOMAIN: The box 1 motif is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Box 1 motif.
APS binding, and STATS binding and activation (By similarity).
Required for STATS/PTPN11/SOCS3 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein, Phosphorylation, Receptor, Signal, Transmembrane, Ubl conjugation.
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Required for ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Subfamily 1. SIMILARITY: Contains 1 fibronectin type III domain.
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Extracellular (Potential)
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InterPro; IPR009167; EPO_receptor.
InterPro; IPR009167; FN_III.
InterPro; IPR00957; FN_III.like.
InterPro; IPR008957; FN_III-like.
InterPro; IPR008959; FN_III-like.
Pfam; PF00041; fn3; 1.
PRGFG PF00060; FN3; 1.
PROSITE; PS01952; HEMATOPO_REC_L_F1; IPROSITE; PS01952; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
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SEQUENCE FROM N.A. (ISOFORM EPOR-F).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse cDNA sequences.
   musculus (Mouse)
                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCFWEEAGSAGVGPEDYSFSYQLEGEPWKPCHLHQGPTARGSVRFWCSLPTADTSSFVPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELRVT-AASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIR 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 HKGNFQLWLYQTDGCLWWSPCTPFAEDPPAPLEVLSERCWGVTQAVEPAADDEGSLLEPV 360
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                                                          (by JAK2)
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; Pred. No. 6e-151;
17; Mismatches 6:
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                                                          Phosphotyrosine
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84.5%;
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Matches 430; Conservative
 458
455
62
107
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453
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             SITE
DISULFID
DISULFID
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SEQUENCE FROM N.A. (ISOFORM EPOR-F).

STRAIN=C578L/6J, and FVB/N-3; TISSUB=Breast tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhale N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhale N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Redriguez A.C., Grimwood S.J.M., Marra M.A.,

Butterfield W.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Redriguez A.C., Grimwood S.J.M., Marra M.A.,

Redriguez A.C., Grimwood S.J.M., Marra M.A.,
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                                                                                                                                                      TISSUE=Erythroleukemia;
MEDLINE=89195238; PubMed=2539263; DOI=10.1016/0092-8674(89)90965-3;
D'Andrea A.D., Lodish H.F., Wong G.G.;
"Expression cloning of the murine erythropoietin receptor.";
Cell 57:277-285(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Erythroleukemia;

WINDININE>2017082; PubMed=1656233;

Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;

Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;

"Unregulated expression of the erythropoietin receptor gene caused insertion of spleen focus-forming virus long terminal repeat in a mirine erythroleukemia cell line ";

Mol. Cell. Biol. 11:5527-5533(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM EPOR-F), AND ALTERNATIVE SPLICING DUE FRIEND SPLEEN FOCUS-FORMING VIRUS.
                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE-90281158; PubMed-2162479; Voussoufian H.D., Lodish H.F.; Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.; Structure and transcription of the mouse erythropoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION IN ERYTHROPOIETIN-INDUCED MITOCENESIS, AND MUTACENESIS GLN-304; TRP-306; SER-317; GLU-324; LEU-330 AND GLU-331. MEDLINE=93180826; PubMed=8382775; Miura O., Cleveland J.L., Ihle J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91201146; PubMed=1849897;
Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.
Gisselbrecht S., Cartron J.-P.;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS EPOR-F AND EPOR-S).
STRAIN=BALB/c; TISSUE=Erythroleukemia, and Liver;
MEDLINE=91080149; PubMed=2175360;
Kuramochi S., Ikawa Y., Todokoro K.;
"Characterization of murine erythropoietin receptor genes.";
J. Mol. Biol. 216:567-575(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Spleen focus-forming virus long terminal repeat insertional activation of the murine erythropoletin receptor gene in the friend leukemia cell line.";
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similarity)
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      Neel B.G.,
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PubMed=7889566; DOI=10.1016/0092-8674(95)90351-8;

Klingmueller U., Lorenz U., Cantley L.C., Neel B.G., Lodish H.F.;

"Specific recruitment of SH-PTP1 to the erythropoietin receptor causes inactivation of JAK2 and termination of proliferative signals.";

Cell 80:729-738(1995).
                                                                                                                                                                                                             Miura O., Nakamura N., Quelle F.W., Witthuhn B.A., Ihle J.N., Aoki N., "Erythropoletin induces association of the JAK2 protein tyrosine kinase with the erythropoietin receptor in vivo."; Blood 84:1501-1507(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH PTPN11, AND MUTAGENESIS OF TYR-367; TYR-425; TYR-453;
TYR-455; TYR-467; TYR-484; TYR-488 AND TYR-503.
PubMed=8639815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gobert S., Chretien S., Gouilleux F., Muller O., Pallard C., Dusanter-Fourt I., Groner B., Lacombe C., Gisselbrecht S., Mayeux P., "Identification of tyrosine residues within the intracellular domain of the erythropoietin receptor crucial for STAT5 activation."; EMBO J. 15:2434-2441(1996).
Inactivation of erythropoietin receptor function by point mutations in a region having homology with other cytokine receptors.", 401. Cell. Biol. 13:1788-1795(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tyrosine 425 within the activated erythropoietin receptor binds Syp, reduces the erythropoietin required for Syp tyrosine phosphorylation, and promotes mitogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH STATS, AND MUTAGENESIS OF ARG-153; GLN-304; TRP-306; SER-317; GLU-324; LEU-330; GLU-331 AND TYR-367.
                                                                                                                                                                                                                                                                                       INTERACTION WITH PTPN6, AND MUTAGENESIS OF TYR-453; 453-TYR--1YR-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quelle F.W., Wang D., Nosaka T., Thierfelder W.E., Stravopodis D., Weinnetein Y., Ihle J.N.;
"Exythropoietin induces activation of Stat5 through association with specific tyrosines on the receptor that are not required for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The adapter protein APS associates with the multifunctional docking
                                                                                                                                                                               INTERACTION WITH JAK2, PHOSPHORYLATION, AND MUTAGENESIS OF TRP-306
                                                                     ALA-224; TRP-235 AND SER-236,
PubMed=8617735; DOI=10.1074/jbc.271.9.4699;
Hilton D.J., Watowich S.S., Katz L., Lodish H.F.;
"Saturation mutagenesis of the WSXWS motif of the erythropoietin
                                                          THE WSXWS MOTIF, AND MUTAGENESIS OF TRP-232; SER-233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION, AND STATS ACTIVATION.
PubMed=11290583; DOI=10.1182/blood.v97.8.2230;
Barber D.L., Beattie B.K., Mason J.M., Nguyen M.H.-H., Yoakim M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21413951; PubMed=11443118; DOI=10.1074/jbc.M102924200; Arai A., Kanda E., Nosaka Y., Miyasaka N., Miura O.; "Crkl is recruited through its SH2 domain to the erythropoietin receptor and plays a role in Lyn-mediated receptor signaling."; J. Biol. Chem. 276:33282-33290(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tauchi T., Damen J.E., Toyama K., Feng G.-S., Broxmeyer H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wollberg P., Lennartsson J., Gottfridsson E., Yoshimura A.,
Ronnstrand L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22510236; PubMed=12444928; DOI=10.1042/BJ20020716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sites Tyr-568 and Tyr-936 in c-Kit.";
Biochem. J. 370:1033-1038(2003).
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                                                                                                                                                  Biol. Chem. 271:4699-4708(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lood 87:4495-4501 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitogenic response.";
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                                                                                                                                                                                               PubMed=8068943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8665851;
                                                          FUNCTION OF
                                                                                                                                      receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00
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Comment=Additional isoforms seem to exist;
Name=EPOR+F; Synonyms=Membrane-bound form;
Isold=P14753-1; Sequence=VSP 009512, VSP 009513;
Isold=P14753-2; Sequence=VSP 009512, VSP 009513;
Isold=P14753-2; Sequence=VSP 009512, VSP 009513;
-1- TISSUE SPECIFICITY: Expressed in relatively mature erythroid progenitor cells and in EPO-responsive erythrolaukemia cells.
-1- DOMAIN: The WSXWS mocif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cellsufface receptor binding is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDKLRVPLWPRVGPLCLLLAGAAWAPSPSLPDPKFESKAALLASRGSEELLCFTQRLEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VCFWEEAASSGM-DFNYSFSYQLEGESRKSCSLHQAPTVRGSVRFWCSLPTADTSSFVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 EVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 EVDVSAGNRAGGTQRVEVLEGRIECVLSNLRGGTRYTFAVRARMAEPSFSGFWSAWSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKOKIWPGIPSPESEFEGLFTTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
"A common epitope is shared by activated signal transducer and activator of transcription-5 (STATS) and the phosphorylated erythropoietin receptor: implications for the docking model of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.1%; Score 2174.5; DB 1; Length 507; 81.7%; Pred. No. 2.4e-143; tive 24; Mismatches 68; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Districtly.
SUBSCELLULAR LOCATION: Type I membrane protein (isoform 1)
Secreted (isoform 2).
ALTERNATIVE PRODUCTS:
                                                                                                                                     C-GLYCOSYLATION, MUTAGENESIS OF SER-233 AND ALA-234, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.78
Matches 415; Conservative
                                                                       Blood 97:2230-2237(2001).
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induced erythroblast proliferation and differentiation. Upon EPO
stimulation, EPOR dimerizes triggering the JAK2/STATS signaling
cascade. In some cell types, can also activate STAT1 and STAT3.
May also activate LYN tyrosine kinase (By similarity).
-!- SUBMNIT: Forms homodimers on EPO stimulation. The tyrosine-
phosphorylated form interacts with several SH2 domain-containing
proteins including LYN, the adapter protein APS, PTPN6, PTPN1,
JAK2, PI3 kinases, STATSA/B, SOC3 and CRKL. The N-terminal SH2
domain of PTPN6 binds Tyr-453 and inhibits signaling through dephosphorylation of JAK2. APS binding also inhibits the JAK-STAT
signaling. Binding to PTPN11, preferentially through the N-
terminal SH2 domain, promotes mitogenesis and phosphorylation of
PTPN11. Binding of JAK2 (Lircugh its N-terminal) promotes cell-
PTPN11. Binding of JAK2 (Lircugh its N-terminal) promotes cell-
surface expression. Interaction with the ubiquitin ligase NOSIP.
                                                                                                                                                                                 + 10 PSSFEYTILDPSSQLLCPRALPPELPPTPPHLKYLYLVVSDSGISTDYSSGGSQGVHGDS
                                                                   SEHAQDTYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS
                                                                                            SEHAQDIYLVLDKWILPRIPCSENLSGPGGSVDPVTWDEASETSSCPSDLASKPRPEGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface expression. Interaction with the ubiquitin ligase NOSIP mediates EPO-induced cell proliferation. Interacts with ATXN2L (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMad=9029168; DOI=10.1016/S0304-3835 (96) 04544-2;
Fujita M., Takahashi R., Kitada K., Watanabe R., Kitazawa S.,
Ashoori F., Liang P., Saya H., Serikawa T., Maeda S.;
"Alternative splicing of the erythropoietin receptor gene correlates
with erythroid differentiation in rat hematopoietic and leukemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional erythropoietin receptor of the cells with neural characteristics. Comparison with receptor properties of erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F., Tabira
Sasaki R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoid=007303-1; Sequence=Displayed;
Name=EPOR-S; Synonyms=Soluble form;
Isoid=Q07303-2; Sequence=VSP_009514, VSP_009515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
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Name=EPOR-F; Synonyms=Full-length form;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS EPOR-F AND EPOR-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CT2-2004 (Rel. 45, Last amnotation update)
Erythropoietin receptor precursor (EPO-R).
                                                                                                                                                                                                                                                                                                                                                                                              507 AA
                                                                                                                                                                                                                                                                SDGPYSHPYENSLVPDSEPLHPGYVACS 507
                                                                                                                                                                                                                                            SDGPYSNPYENSLIPAAEPLPPSYVACS 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells.";
J. Biol. Chem. 268:11208-11216(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93266574; PubMed=7684373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissue=Pheochromocytoma;
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Q07303;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE SPECIFICITY: Both isoforms expressed in bone marrow, spleen and eythnoleukemia cell lines.

DOMAIN: The WXXWS most appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IFR008957; FN_III-like.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003528; HemptreceptL_F1.
Pfam; PF00041; fn3; 1.
PROSTE; PSS0851; FN3; I.
PROSTE; PSS0853; FN3; I.
PROSTE; PS01352; HRWATOPO REC_L_F1; 1.
Alternative splicing; Glycoprotein; Phosphorylation; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Required for STAT5/PTPN11/SOCS3 binding.
                                       receptor binding. The box 1 motif is required for JAK interaction and/or \ensuremath{\mathsf{The}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Box 1 motif.
APS binding, and STATS binding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
Fibronectin type-III.
Required for ligand binding (Esimilarity).
WSXWS motif.
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Erythropoietin receptor.
Extracellular (Potential)
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PIR, A46713; A46713.
HSSP, P19235; IEBA.
RGD; 2560; Epor.
InterPro; IPR001996; Cytkn_recept_B/G.
InterPro; IPR009167; EPO_receptor.
InterPro; IPR009167; EPO_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Ubl conjugation.
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68 ASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAA
                                                                                                                                                                                                                                                                                                                                                                         128 -SGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                       63 SSGASRYRRTIHVNEVVLLDPPARLVARRADEGGHVVLRWLPPPGAPMASLIRYEVNISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLDPLILTLSLILVVILVLLTVLALLSHRRALKOKIWPGIPSPESEFEGLFTTHKGNFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 DLDPLILTLSLVLVLILLLLAVLALLSHRRTLKOXIWPGIPSPESEFEGLFTTHKGNFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 WLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVGSEHAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 WLYQTDGCLWWSPSTPFPEDPPAPLEVLSECCWGVTQAVEPGADDGGSLLEPVGSEHAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 TYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGASAASFEY
                                                                                                                                                                                                                                                                                                                      Gaps
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
Erythropoietin receptor (Fragment).
Erythropoietin seceptor (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae; Caprinae; Ovie.
                                                                                                                                                                                                                                                                                                                      1;
David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RMEJ, A7029235, AAK38737.1; -.
RHSP; P19235; JEBA.
RGO; GO:0004872; F:receptor activity; JEA.
RICEPTO; JER003961; FN III.
RICEPTO; JER003528; HemptreceptL_F1.
FEAM; PRO0401; fn3; 1.
REART; SM00060; FN3; 1.
REART; PS50853; FN3; 1.
RROSITE; PS50853; HEMATOPO_REC_L_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                     DB 2; Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Indels
                                                                                                                                                                                                                    1 1
387 387
387 AA, 42039 MW, ODIE6173C432EBC6 CRC64;
                                                                                                                                                                                                                                                                                  61.5%; Score 1670.5; DB 2, 82.9%; Pred. No. 2.4e-108; ative 14; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AY029231; AAK38170.1; -.
HSSP, P19235; 1EBA.
GO; GO:0004872; F:receptor activity; 1EA.
InterPro; IPR003951; FN III.
InterPro; IPR003558; HemptreceptL_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILDPSSQLLRPWTLCPELPPTPPH 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TILDPSSQLLRPRALPPELLPTPH 387
                                                                                                                                                                                                                                                                                                                    Matches 319; Conservative
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                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                   Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGL 480
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                  similarity).

Abosphotyrosine (by JAK2) (By similarity).

Phosphotyrosine (by JAK2) (By similarity).

Similarity).

DLDPLILTLSLILL -> GPATYPRGGGGAGPNTS

KPP (in isoform EPOR-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 SLLTASDLDPLILTLSLILVLISLLLTVLALLSHRRALROKIWPGIPSPENEFEGLFTTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILTPSDLDPLILTLSLILVVILTVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG
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                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2004 (TrEMBLrel. 26, Last annotation update)
Erythropotetin receptor (Fragment).
Ovis aries (Sheep).
Eukaryotas, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis
                                                                                                                                                                                                                                                                                   DB 1; Length 507;
                                                   (By
                                                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                             266 507 Missing (In isoform EPOR-S)
/FIId=VSP 009515.
507 AA; 55499 MW; AC79AF22D06A7312 CRC64;
                 Phosphotyrosine (by JAK2) similarity).
                                                   Phosphotyrosine (by JAK2)
                                                                                                                                                                                   KPP (in isoform EPOR-S).
                                                                                                                                                                                                                                                                                  Query Match 79.3%; Score 2152.5; DB 1
Best Local Similarity 80.5%; Pred. No. 8.2e-142;
Matches 409; Conservative 31; Mismatches 67;
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     similarity)
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                    467
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265
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                  467
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Q27950;
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                                                                                                                                                                                                                                                                          68 ASAGVGPGNYSFSYQLEDBPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAA 127
                                                                                                                                                                                                                                                                                                                                                           -SGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 DLDPLILTLSLILVVILVLLTVLLTSHRRALKQKIWPGIPSPESEFEGLFTTHKGNF-- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...----QLWLYQNDGCLWWSPCTPFTEDPPASLEVLS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GGLVVPSRPGASLLLWPNSKSLSKLVLFPQLWLYQTDGCLWWSPSTPFPEDPPAPLEVLS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ERCWGTMQAVEPGTDDEGPLLEPVGSEHAQDTYLVLDKWLLPRNPPSEDLPGPGGSVDIV 395
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 AMDEGSEASSCSSALASKPSPEGASAASFEYTILDPSSQLLRPWTLCPELPPTPPH 451
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11ntron 5-inserted form of erythropoietin receptor precursor.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=98296111; PubMed=9630610; DOI=10.1016/S0167-4889(98)00037-8; Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H., Miyatake K., Nakami Y.; Takenoshita M., Tsuyama S., Inui H., "The intron 5-inserted form of rat erythropoietin receptor is expressed as a membrane-bound form "; Blochim. Blophys. Acta 1403:169-178(1998).

Binchim. Biophys. Acta 1403:169-178(1998).
                                                                                                                                                                                                                                         32;
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GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain.
GO; GO:0004892; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; HemptreceptL_F1.
Fnam; PF00041; fn3; 1.
SWART; SM00060; FN3; 1.
                                                                                                                                                                                                 Length 418;
                                                                                                                                                                                      Query Match
60.6%; Score 1645; DB 2; Length 41
Best Local Similarity 76.7%; Pred. No. 1.6e-106;
Matches 319; Conservative 14; Mismatches 51; Indels
                                                                                                                                                   BB742EBEA034503C CRC64;
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS50833; FN3; 1.
PROSITE; PS01352; HEWATOPO_REC_L_F1; UNKNOWN_1.
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418 418
418 AA; 45282 MW;
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                                                                                 Receptor.
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                                                                                                                                                                                                                                               61 VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL
                                                                                                                                                                                                   SLLTPS------DLDPLILTLSLILVVILVLLTVLALLSHRR---ALKQKIWPGIP
                                                                                                                                                                                                                                                                                                                 ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.0%; Score 1058; DB 2; Length 316; Best Local Similarity 68.6%; Pred. No. 9.9e-66; Matches 212; Conservative 23; Mismatches 60; Indele 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 229;
                                           1 24 Potential.
25 316 Potential.
316 AA; 34220 MW; 05C44BF8516C180B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AA; 25196 MW; FGEO1C4AB07893E8 CRC64;
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01, Last sequence update)
26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50853; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
PS50853; FN3; 1.
PS01352; HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erythropoietin receptor (Fragment)
Name=EpoR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Best Local Similarity
                               Receptor; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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NCBI_TaxID=9915;
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PRELIMINARY;
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                                                                                      OGUAP7,
OGUAP7,
05-JUL-2004 (
                                                                                                                                                                                                          Name=CRFA9;
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                                                                                                                                                                                                RYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSE 238
                                                                                                                    119 PLELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHI 178
                                                                                                                                         61 PLELHVTAASGASRYRKTIHVNEVVLLDPPARLVARRADEGGHVVLRWLPPPGAPMASLI 120
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                                                             1 DLVCFWEEAATAGVGFDNYSFSYQLEGEPWKPCRLHQAPTARGLVRFWCSLPTADTSSFV
                                     DLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFV
                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 PLELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                239 PVSILTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIP 287
                                                                                                                                                                                                                                                                                                       PVSLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.2%; Score 1011; DB 2; Length 229; 84.3%; Pred. No. 1.3e-62; Live 10; Mismatches 26; Indels
    26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Bone marrow;
Suliman H.B., Feldman B. F, Majiwa P.A.O., Logan-Henfrey
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; UG1399, AAB03971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
25170 MW; EDFAA6F110D992E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0853; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR00857; FN III-like.
InterPro; IPR003589; Hemptrecepti_FI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NAR-2004 (TrEMBLrel. 26, Last ann
Erythropoietin receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 64.51
Matches 193; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00041; fn3; 1
SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AA;
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NCBI_TaxID=9913;
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229
Matches 194;
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NON TER
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Deguence FROM N.A.

Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Muccell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Luttalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Blimont C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Rarra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Muncker P., Lander E.S., Weissenbach J., Crollius H.R.;
"Analysis of the Tetraodon nigrovitidis genome reveals the
protokaryotype of bony vertebrates and its duplication in teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 GCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEP------ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 LCLLLAGAAWAPPPNLPDPK-PESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 PGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 VDQYTFTYAYQNENSSRCPLKSISAADSKRLFICHLNR--IKMFVQMDIQV-HREGMLIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 HRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 QRVEILEGRIECVLSNIRGRIRYTFAVRARMAEPSFGGFWSAWSEPVSLLT-PSDLDPLI
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                                                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 AA; 59609 MW; C4A04BFC94E9C3B6 CRC64;
                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Class I helical cytokine receptor number 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY374481; AAR25672.1; -.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR003996; Cytha recept_B/G.

InterPro; IPR003961; FN III.

InterPro; IPR003561; FN III.-like.

InterPro; IPR003528; HemptreceptL_F1.

PRomir; SM00060; FN3; 1.

PROSITE; PS50853; FN3; 1.

PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
PRT;
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                                    380
356 GLVERRKVEAHSAVSEGWEVTADNQMPTDSWRGPQPNGVPCSRSPLLESQDAYVTLSTNN 415
                                                                                  ------PSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEG---ASAASFEYT 427
                                                                                                          OREEEPLNHIPEETLP----IEKLFTSRKOICESHSDLGSMQOSPASSHLSSQSSFE-- 468
                                                                                                                                 428 ILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGLSDGPYSN 487
                                    -------RNP-----RNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Melanoma; MEDLINE=S6115587, PubMed=8666384; MEDLINE=S6115587, PubMed=8666384; MEDLINE=S6115587, Van Roost E., Arden K.C., Vermeesch J.R., Weiss S., Godelanie D., Flint J., Lurquin C., Szikora J.P., Higgs D.R., Marynen P., Renauld J.C., Szikora J.P., Higgs D.R., "The IL-9 receptor gene (IL9R): genomic structure, chromosomal localization in the pseudoautosomal region of the long arm of the sex chromosomes, and identification of IL9R pseudogenes at 9qter, 10pter, 16pter, and 18pter ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BEDLINE-94250901; Pubmed-8193355;
Chang M.S., Engel G., Benedict C., Basu R., McNinch J.;

"Isolation and characterization of the human interleukin-9 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20122249; PubMed=10655549; DOI=10.1093/hmg/9.3.395; Ciccodicola A., D'Esposito M., Esposito T., Gianfrancesco F., Miano M.G., Mararazzo M.R., Vacca M., Franze A., Cuccurese M., Cocchia M., Curci A., Terracciano A., Torino A., Cocchia M., Cocchia M., Torino A., Cocchia M., D'Urso M.; Archidiacono N., Rocchi M., Chiessinger D., D'Urso M.; Differentially regulated and evolved genes in the fully sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=92302307; PubMed=1376929; Acrmounl A., Houssiau F., Uyttenhove C., Vermauld J.C., Drucaz C., Kermounl A., Houssiau F., Uyttenhove C., van Roost E., van Snick J.; Expression cloning of the murine and human interleukin 9 receptor
                                                                                                                                                                                                                                                                                                                                                                                       Lucia Sagrama (Aradama).
Lucia Sagrama (Aradama).
Mammalja; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694 (1992)
                                                                                                                                                                                                                                                                  ILGR HUMAN STANDARD; PRT; 522 AA. 001113; Q14634; Q8WWU1; Q96TF0; 01-APR-1993 (Rel. 25, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 105-UUJ-2004 (Rel. 44, Last annotation update) Interleukin-9 receptor precursor (IL-9R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xq/Yq pseudoautosomal region.";
Hum. Mol. Genet. 9:395-401(2000).
                                                                                                                                                                                                                                                                                                                                                                    Name=IL9RY; Synonyms=IL9R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 29:371-382(1995).
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                  488 PYENSL 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 RGPEE--LLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAP---- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 OGPRSRIFICLINNILRIDCHW-SAPELGOG-----SSPWLLFTSNOAPGGTHK 94
                     164; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the type I cytokine family of receptors
                                                                                                                                                                                                                                                                                      surface receptor binding. DOMAIN: The box 1 motif is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 N-linked (GICNAC. .) (Potential).
156 N-linked (GICNAC. .) (Potential).
239 F -> Q (in dbSNP:6522).
7/FIGH=VAR 014804.
331 G -> R (in Ref. 1 and 2).
439 Missing (in Ref. 3 and 4).
57233 MW, BBB73D6E2FAE37CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 300007; -.
G0; G0:0005815; C:extracellular space; TAS.
G0; G0:0005887; C:integral to plasma membrane; TAS.
G0; G0:0004919; F:interleukin-9 receptor activity; TAS.
G0; G0:0004919; F:interleukin-9 receptor activity; TAS.
G0; G0:0001165; P:isignal transduction; TAS.
InterPro; IPR002996; Cyrkn_recept_B/G.
InterPro; IPR003996; Cyrkn_recept_B/G.
InterPro; IPR003997; FN III-like.
InterPro; IPR003997; FN III-like.
InterPro; IPR003931; HemptreceptS F1.
Glycoprotein; Polymorphism; Receptor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 251; DB 1; Length 522; 25.9%; Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                           Subfamily 4.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-9 receptor.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic (Potential). Fibronectin type-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poly-Asn.
WSXWS motif.
Box 1 motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poly-Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, M84747; AAA58679.1; -. EMBL, S71404; AAB30844.2; ALT_SEQ. EMBL, S71420; AAD14081.1; -. EMBL, L39064; AAAC29513.1; -. EMBL, AAZ71736; CAB96817.1; -. EMBL, AY071830; AAL55435.1; -. EMBL, B45268; B45268. MIM, 30007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 25.9
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 4
522 AA;
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FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  activation.
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54 GTÝQLLYAYRGEKPRACPLYSQSVPTFGTRYVCQFPAQDEVRLFFPLHLWVKNVSLNQTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 IQRVLFVDSVETCCPTLWMPNPVPVLDQPPCVHPTASQPHGPVRTSPAGEAPFLTVKGGS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 COWQQODRISSQGFFRHSRIRCCPIDRDPIWEKCEEEEPRPGSQPALVSRCHFKSRNDSV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYQLRYTGEGREDWKVLEPSLGARGGTLELRPRARYSLQLRARLNGPTYQGPWSAWSPPA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SLLTPSDLDPLILTLSLILVVILVLLTVLALL----SHRRALKQKIWPGIPSPESEFFG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 GNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTAD-TSSFVPLELRVTAAS-GAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 CLVSGLQAGKSYWLQLRSQPDGVSLRGSWGPWSFPVTVDLPGDAVTIGLQCFTLDLKMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-----VLS----VLS-----VLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                                                                                                                                                                                                                      SEGUENCE FROM N.A.
MEDLINE-21992449; Pubmed=11997107; DOI=10.1016/S0167-4781(01)00357-8;
Sabath PF., Lofton-Day C., Lin N., Lok S., Kenneth Kaushansky.,
Broudy V.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 CLLLIAGAAWAPPPNLPD-PKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CLLLA------LPNOAQVTSQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 224; DB 2; Length 566;
21.8%; Pred. No. 3e-07;
ive 42; Mismatches 167; Indels 250; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 IHILVEVTTAQGAVHSYLGSPFWIHQAVLLPTPSLHWREVSSGRLELEWQHQSSWAAQET
                                                                                                                                                                                                                                                                                                                                                                                                                                           an isoform of murine Mpl.";
                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRYEVDVSAGNGA------GSVQRVEILEGRTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50853; FN3; 1.
PROSITE; PS00852; HEMATOD REC L F1; UNKNOWN 1.
PROSITE; PS00041; HTH ARAC FAMILY 1; UNKNOWN 1.
SEQUENCE 566 AA; 63339 WW, A19030DSF7BDBA6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 YHRVIHI------NEVVILDAP------
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VGLVA-----RLADESGHVVLR--WLP-----
                                                                                                                                                                        566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:97076; Mpl.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       219 AVRARMAEPSFGGFWSAWSEPVSLLTP 245
                                                                                    241 QVRSKPDGTSMDGVWGPWSEVVVAETP 267
                                                                                                                                                                                                         Created)
                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 128; Conservative
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                        Name=Mpl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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Q925FS
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                                                                                                                              202 VGVTWLILEAFELDPGFIHEARLRVQMATLEDDVVEEERYTGQWSEWSQPVCFQAPQRQG 261
                                                                                                                                                                                      320 NGNFQTWMGAHGAGVLLSQDCAGTPQGALEPCVQEATALLICGPARPWKSVALEE---EQ 376
                                                                                                                                                                                                                                                                                                                           ---- 144
                             VVLLDAPVGLVARLADESGHVVLRW-LPPPETPMTSHIRYEVDVSAGNGA-GSVQRVEIL 199
                                                  200 EGRIECVLSNLRGRIRYTFAVRAR-------MAEPSFGGFWSAWSEPVSLLTPSDLD 249
                                                                                                                                                                 PLILTL----SLILVVILVLLT----VLALLSHRRALKOKIWPGIPSPESEFEGLFTTH 300
                                                                                                                                                                                                                                 301 KGNFOLWL-YQNDGCLWWSPCT-----PFTEDPPASLEVLSERCWGTMQAVEPGTDD 351
                                                                                                                                                                                                                                                                                                    EGPLLEPVGSEHAQD-----TYLVLDKWLLPRNPPSEDLPGPGGSVDIVAM 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 VGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRV-TAASGA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 PRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPP-------PETPMT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 I----HRFYYW--DAP-TICAVSTQRSGVSGMRHICVFPSQDVRLFTPLHVLVLDTTTNR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 WAP------PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bartunek P., Karafiat V., Bartunkova J., Dvorakova M., Kralova J., Bartunek P., Karafiat V., Bartunkova J., Dvorakova M., Kralova J., Subjer P., Zenke M., Dvorak M., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AX613435, AAT45555.1; -
EMBL, AX613435, AAT45555.1; -
EMBL, AX613435, AAT45555.1; -
InterPro; IPR003951; F. III-like.

InterPro; IPR008957; FN_III-like.

SMART; SM000601; FN3; 2.

PROSITE; PS50853; FN3; 1.
CILRGSE---CTVVLPPEAVLVPSDNFTITFHHCMSGREQVSLVDPEYLPRRH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 AA; 68856 MW; 9E8FCC6CE61E0EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 231.5; DB 2;
26.6%; Pred. No. 1e-07;
iive 32; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 AA
                                                                                                                                                                                                                                                                                                                                                                                        427 -EGSRSSSSSSS 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gallus (Chicken)
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es 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                               142
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Best Local S
Matches 71
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NCBI_TaxID=9860;
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028235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=PRLR;
                                                                                    SITE
DISULFID
DISULFID
CARBOHYD
 DOMAIN
TRANSMEM
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CONFLICT
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                                                                                                                                       CARBOHYD
                         DOMAIN
DOMAIN
DOMAIN
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PRLR_CEREL
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MEDLINE=97468290; PubMed=9321486;
MEDLINE=97468290; PubMed=9321486;
Wincent A.L., Wang L., Tuggle C.K., Robic A., Rothschild M.F.;
Prolactin receptor maps to pig chromosome 16.";
Mamm. Genome 8:793-794(1997)
-!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding (By similarity).
-!- DOMAIN: The box 1 motif is required for JAK interaction and/or
                                      LFTTHKGNFQLWLYQNDGCLWWSPCTPFTED----PPASLEVLSERCWGT---MQAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation.
SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 1.
                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                        Irott J.F., Hovey R.C.;
"Cloning and characterization of multiple forms of the pig (Sus
                                                                                     348 GIDDEG-----PLLEPVGS----EHAQDTYLVLDKWLLP 377
                                                                                                              520 QMDYRGLQPCLRTMPLSVCPPMAETGSCCTTHIANHSYLPLSYWQQP 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subfamily 1. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
Glycoprotein; Receptor; Repeat; Signal; Transmembrane. SIGNAL 1 24 Potential.
CHAIN 25 625 Prolantin recent.
                                                                                                                                                                                    06JTA9; 046679; 06JTA9; 06JTB0;
25-0CT-2004 (Rel. 45, Created)
25-0CT-2004 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                           625 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U96306; AAC02897.1; -...
InterPro; IPR002296; Oykkn.recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003528; Hemptrecepti_F1.
Pfam; PF00041; fn3; 2.
SWART; SW00060; FN3; 2.
                                                                                                                                                                                                                                        Prolactin receptor precursor (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY308824; AAQ76841.1; -.
EMBL; AX308825; AAQ76842.1; -.
EMBL; AX308826; AAQ76843.1; -.
                                                                                                                                                                                                                                                                                                                                          STRAIN=Landrace, and Yucatan;
                                                                                                                                                                                                                                                                                                                                                                                   prolactin receptor.";
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Sus scrofa (Pig)
                                                                                                                                                                                                                                                      Name=PRLR;
                                      596
                                                                                                                                                                           PRLR PIG
                                                                                                                                                  RESULT 14
PRLR PIG
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255 LSLIL-----VVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH---KGNFQL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 PWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTA-----ASGAPRYHRVIHIN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TF----THECPDYKTGGPNSCYFNKKHTSIWTIYIITVNATNOMGSSSSDPRY---VDVT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 EVVLLDAPVGLVARL---ADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DQQLMPAH--SKEHPSQGRKPTHLDPDSDSGRGSCDSPSLLSEKCDEPRANPPK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 YİVEPDPEVNLTLELKKPEDQKPYLMIKMLPPTLVDVRSGWLTLQYEIRLQPEKTA--EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 PPGKPE------IFKCKSPEK------FTFTCWWKPGADGGL-PTNYTLTYHKEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 RVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLDPLILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 WLYQNDGCLWWSPCTPFTEDPPASLEVLSE-RCWGTMQAVEPGTDDEGPLLEPVGSEHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 DIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSS-----ALASKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.1%; Score 220; DB 1; Length 625;
23.8%; Pred. No. 6.4e-07;
iive 65; Mismatches 179; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SPEGASAASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGIST 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 FHTPEGIEKPG-----DPETNLPRP----ODPOSTSVESKLLYFHADGSKSST 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervidae,
                                                                                                                                                                                                                                                                                                                                   Potential).
                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                       P -> R (in Ref. 1; AAQ76842).
L -> P (in Ref. 1; AAQ76842).
K -> G (in Ref. 1; AAQ76842).
K -> R (in Ref. 1; AAQ76842).
M -> L (in Ref. 1; AAQ76842).
G -> S (in Ref. 1; AAQ76842).
S -> G (in Ref. 1; AAQ76842).
W; 751B2B593ABFCS1B CRC64;
Extracellular (Potential)
                                               Cytoplasmic (Potential). Fibronectin type-III 1. Fibronectin type-III 2.
                                                                                                                                                                                                                   By similarity.
By similarity.
N-linked (GloNAc..
N-linked (GloNAc..
N-linked (GloNAc..
P-> R (in Ref. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                           WSXWS motif.
Box 1 motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prolactin receptor precursor (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seqn
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervus elaphus (Red deer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 113; Conservative
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86 CYPSKKHTSIWKIYVITVNAINQMGVSSSDPLY---VDVTYIVEPEPPANLTLELKHPED 142

CSLPTADISSFVPLELRVTA----ASGAPRYHRVIHINEVVLLDAPVGLVARL---AD 157

107

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158

31 PKIIKCRSPGKETFTCWWEPGSDGGL-PTNYTLTYHKEGE----TLIHECPDYKTGGPNT 85

143 RKPYLWIKWFPPTLTDVKSGWFMİQYEIRLKPETAAD--WEIHFAAKQTQLKIFSLYPGQ 200

ESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRT 214

215 RYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDL---DPLILTLSLILVVILVLLTVLAL

272 LSHRRALKOKIWPGIPSPESEFEGLFTTHKGNFQLWLYQNDGCLWWSPCTPFTEDPPASL 331

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EVLSERCWGTMQAVEPGTDDEGPLLEPVGSEHAQDTYLVLDKWLLPRNPPSEDLPGPGGS 391 297 E-----SQDFPPTSDCEDLLMEFIEVDDSE-----DQQLMPR--PSKEHMEQGVK 339

332

340 PMHMDPDSDSGRGSCDSPSLFSEKCDEPQAHPFKFYTPEDP-EKLENPETNLTCLQAPQS 398

392 VDIVAMDEGSEASSCSS-ALASKPSPEGASAASFEYTILDPSSQLLRPWT--LCPELP--

399 TSREDKIPYFHANGPKSSTWPFPQPPSLHNPRYSYHNIADVCELALGMAGTTATLLDQTD 458

셤 ò

-----TDYSSGDSQGAQGGLSDGPYSNPYENSLIPAAEPLP

-----SGIS----SGIRDHT---KYLVVSD-----SGIS-----

465

296

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                     SUBCELLUIAR LOCATION: Type I membrane protein.
DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-burface receptor binding.
BUMAIN: The box I motif is required for JAK interaction and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSI ::
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GO; GO:00042978; F:ornithine decarboxylase activator activity; ISS.
GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.
GO; GO:0042978; F:ornithine decarboxylase activity; ISS.
GO; GO:004925; F:prolactin receptor activity; ISS.
GO; GO:0007166; P:anti-apoptosis; ISS.
GO; GO:0007166; P:anti-apoptosis; ISS.
GO; GO:0007165; P:anti-apoptosis; ISS.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
GO; GO:000717; P:transmembrane receptor protein tyrosine kin. .; I.
RO; GO:000717; P:transmembrane receptor protein; ISS.
R InterPro; IPR003961; FN_III.
R InterPro; IPR003961; FN_III.
                             TISSUE=Liver;
MEDINE=9630311; PubMed=7561644;
MEDINE=96303011; PubMed=7561644;
Clarke L.A., Edery M., Loudon A.S., Randall V.A., Postel-Vinay M.C.,
Kelly P.A., Jabbour H.N.;
"Expression of the prolactin receptor gene during the breeding and
"Expression of the prolactin receptor gene for the
                                                                                                                   non-breeding seasons in red deer (Cervus elaphus): evidence for the expression of two forms in the testis."; J. Endocrinol. 146:313-321(1995).

-!- FUNCTION: This is a receptor for the anterior pituitary hormone.
                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 1 motif.

By similarity.
By similarity.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                  Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
PROMITE: PROMO41; Fn3; 2.
PROSITE; PSO1352; FN3; 2.
PROSITE; PSO1352; HEWATOPO_REC_L_F1; 1.
PROSITE; PSO1352; HEWATOPO_REC_L_F1; 1.
SIGNAL 1 24 By similarity.
CHAIN 25 234 Extracellular (Potential).
PROJECTIN Teceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linked (GlcNAc. .) (Post 1975E47CB63CF28EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X94953; CAA64419.1; -.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 AA;
                                                                                                                                                                                            prolactin.
                                                                                                                                                                                                                                                                                                   activation
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Search completed: April 21, 2005, 08:59:16 Job time : 221.5 secs
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PEBLICFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW 106

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Ouery Match
8.0%; Score 216.5; DB 1; Length 581;
Best Local Similarity 21.6%; Pred. No. 1e-06;
Matches 113; Conservative 80; Mismatches 206; Indels 125; Gaps

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WPI; 1990-260931/34.
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04-JAN-1991
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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geneseqp2003bs:*
geneseqp2004s:*
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1: geneseqp1980s:*
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                                                            protein search, using
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ALIGNMENTS

ARBOLT: ARROFS12 standard; protein; 508 AA.

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AC AAROFS12;
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AC AAROFS12;
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DT 25-MAR-2003 (revised)
DT 25-MAR-2003 (first entry)
XX
B EPO receptor.
XX
MO9008822-A.
XX
MO900882-A.
XX
MO90082-A.

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93US-00106815
                                                          N-PSDB; AAQ82990
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16-AUG-1993;
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Matches 508
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                                                          MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL
                                                                             VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL
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/note= "reverse primer AA082992 specific site"
       Length 508;
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1.9e-216;
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/note= "forward primer AAQ82991
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       Query Match
100.0%; Score 2715;
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 508; Conservative 0; Mismatches
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/note= "extracellular
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/note= "extracellular
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The full-length erythropoietin receptor (EPO-R) is given. Extracellular domains are expressed from vector plasmid pGRX-2T as fuelon proteins with glutathione-S-transferase. The domains acod for investigating the structure of the EPO-R and for identifying factors involved in regulating differentiation and proliferation mechanisms in erythroid progenitor ells. They can also be used for identifying and quantitating EPO and EPO-R as well as in understanding haematopoietic malignancy and some cardiovascular system disorders. (Updated on 25-MAR-2003 to correct PN
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                                                                          New pure human erythropoietin receptor fragment - obtd. by expression a fusion protein having a thrombin proteolytic cleavage site.
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100.0%; Pred. No. 1.9e-216;
ive 0; Mismatches 0;
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                                                                                                                                                                Disclosure; Page 27-29; 42pp; English
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508; Conservative
WPI; 1995-098767/13
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Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbetal,
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241 SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH 300
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                                                          KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG
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09-0CT-2002; 2002US-0417243F-
18-0CT-2002; 2002US-041575F-
08-NOV-2002; 2002US-0424881F-
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N-PSDB; ADO05723.
GENBANK; 4557561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant erythropoletin receptor polypeptide(s) - used for detection, purificn. and therapy and for prodn. of antibodies for detection and
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                                                                                             Erythropoietin receptor; anemia therapy; diagnostic.
                                                                                                                                                                                                                                                                                                                                  'note= "transmembrane region"
                                                                                                                                                                                                                                                                                            "N-glycosylation site"
                                                                                                                                                                                              l. .24
/note= "signal peptide"
                                                                                                                                                                                                                                                       "mature protein"
                                                                                                                                                                        Location/Qualifiers
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                                                        Human erythropoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 9; 24pp; English.
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    (revised)
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76. .79
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N-PSDB; AAQ81892.
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25-MAR-1991;
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  25-MAR-2003
11-AUG-1995
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Matches 508;
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cell response to antigens associated with the condition, such as in an allergic response, an autoimmune disorder, a viral infection, a microbial infection, a parasitic infection or a tumour. The present sequence represents a human erythropoletin receptor (EPOR), preferentially expressed in regulatory T cells.
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                                                                                                                                    ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 180
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                                                                              Gaps
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HIV; AIDS.
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                                                               Length 508;
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                                                             Score 2715; DB 8;
Pred. No. 1.9e-216;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ejection; immune system; rheumatoid
bowel disease; multiple sclerosis;
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                                                           Query Match
Best Local Similarity 100.0%; Primatches 508; Conservative 0;
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2002US-00325899.
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                                                            Query Match
Best Local Similarity
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                                             Sequence 508 AA;
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20-DEC-2002;
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                                                                                                                                                                                                                                                                                                                              The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic shelt, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatof arthritis, lupus, inflammatory bowth diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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        Prentice
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ilarity 100.0%; Pred. No. 1.9e-216;
Conservative 0; Mismatches 0;
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        Woodward R,
     Fry K,
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Wohlgemuth J,
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Best Local Simil
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Tumour-associated antigenic target (TAT) polypeptide PRO34323, SEQ:5259.
                                                                                                                                                                                                                                                                                                                                                                         New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                     Tumour-associated antigenic target; TAT; human, overexpression; cacolorectal diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; blacker cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 5259; 7273pp; English.
 standard; protein; 508 AA
                                                                                                                                                                                                                                                 29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                       32-OCT-2002; 2002US-0414971P
                                           18-NOV-2004 (first entry)
                                                                                                                                                          gene therapy; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer or tumor.
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
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                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                            15-APR-2004.
                     ABM82037;
                                                                                                                                                                                                                                                                                                                    Wu TD,
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polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central mervous system, melanoma and leukaemia. TAT nucleic acids may further be nervous system, melanoma and leukaemia. TAT nucleic acids may further be polypeptides, and their related nucleic acids. The TAT polypeptides are, overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and gene therapy. The present sequence invention relates to human tumour-associated antigenic target used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequen represents a TAT polypeptide of the invention

ô 9 9 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL 1 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL ë, 100.0%; Score 2715; DB 8; Length 508; ilarity 100.0%; Pred. No. 1.9e-216; Conservative 0; Mismatches 0; Indels 0 Query Match Best Local Similarity Matches 508; Conserv

VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCKLHQAPTARGAVRFWCSLPTADTSSFVPL 120 61

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300 300 360 420 61 VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL 120 KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG 360 AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGL 480 421 AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSGAQGGL 480 361 SEHAQDIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS 420 SLITPSDLDPLILTLSLILVVILVLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG ELRVTAASGAPRYHRVIHINEVVILDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY EVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV SEHAQDIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS Human, erythropoietin receptor; EPO receptor; fusion protein; erythropoietin receptor extracellular domain; signal transduction; 508 508 Human erythropoietin receptor SEQ ID NO.5. 481 SDGPYSNPYENSLIPAAEPLPPSYVACS SDGPYSNPYENSLIPAAEPLPPSYVACS Ą. ABB09173 standard; protein; 508 (first entry) JS2002031806-A1 Homo sapiens. 01-JUL-2002 181 receptor. 181 241 241 301 301 361 421 ABB09173; 481 ò g Š g 8 g ò g ò g 合 ò

98US-00016159. 30-JAN-1998; 14-MAR-2002

WPI; 2002-361181/39 (LEEJ/) LEE J Y. Lee JY;

N-PSDB; ABL51519

97US-00876227.

16-JUN-1997;

New purified human erythropoietin receptor polypeptide, useful for studying ligand binding to erythropoietin receptor, as well as for analyzing and understanding receptor structure and signal transduction.

Example 1; Page 11-12; 19pp; English.

The present invention describes a purified human erythropoietin (EPO) receptor polypeptide, which consists essentially of amino acids 25-250 of the full length human EPO receptor protein. The human EPO receptor polypeptide is capable of binding human erythropoietin. Also described is a purified fusion protein comprising essentially of: (a) a first

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05-NOV-2001; 2001US-0338626P.
06-NOV-2001; 2001US-0338626P.
09-NOV-2001; 2001US-034539P.
09-NOV-2001; 2001US-034539P.
15-NOV-2001; 2001US-0335610P.
21-NOV-2001; 2001US-0332152P.
29-NOV-2001; 2001US-0333152P.
29-NOV-2001; 2001US-0333156P.
04-DEC-2001; 2001US-0334300P.
04-DEC-2001; 2001US-033480P.
15-MAY-2002; 2002US-033400P.
16-MAY-2002; 2002US-0331048P.
16-MAY-2002; 2002US-0331148P.
02-JUL-2002; 2002US-0333144P.
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2001US-0338626P.
2001US-0333072P.
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2; 2002US-0401626P.
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PEYMAN J A.
RAGTELLI L.
RIEGER D K.
ROTHENBERG M E.
SHENOY S G.
SHIMKETS R A.
SPADERNA S K.
STARLING G.
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KHRAMTSOV N V.
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GANGOLLI E A.
GERLACH V.
GORMAN L.
GROSSE W M.
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MCQUEENEY K.
MEZES P S.
MILLER C E.
MILLET I.
MISHRA V.
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BOLDOG F L.
BURGESS C E.
CASMAN S J.
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DHANABAL M.
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HACKETT C.
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 segment having a thrombin protectivic cleavage site at the carboxyl terminus; and (b) a second polypeptide segment consisting essentially of the purified human EPO receptor, where the second polypeptide segment is covalently coupled to the carboxyl terminus of the first polypeptide segment. The human EPO receptor polypeptide is useful for studying ligand binding to the EPO receptor and for quantitating the amounts of the EPO receptor and for quantitating the amounts of the EPO receptor and for guantitating the amounts of the EPO receptor structure and signal transduction. The present sequence represents human EPO receptor from the present invention
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polypeptide segment having an amino terminus and a carboxyl terminus, the
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421 AASFEYTILDPSPQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSOGGOGGL 480
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361 SEHAQDTYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS
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1 VL, Gorman L;
Khramtsov NV;
Mazur A, Mcque
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28-MAY-2002; 2002US-0383534P.
28-MAY-2002; 2002US-0383744P.
29-MAY-2002; 2002US-0383829P.
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31-DEC-2001; 2001US-0344903P.
17-APR-2002; 2002US-0373288P.
15-MAY-2002; 2002US-0380981P.
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31-OCT-2002; 2002US-00287971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis, hypertension, pulmonary stenosis, scleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease, anorexia and immune disorders. This sequence represents a human NOVX polypeptide of the invention. Note: The sequence data for this patent is also available from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AVDVSAGNGAGSVQRVKILEGRTECVLSNIRGRTRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDHLGASIWPQVGSLCLLPPAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 54; 330pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.2
Matches 504; Conservative
                                                                                     VERNET C A M.
ZERHUSEN B D.
VOSS E Z.
ZHONG M.
                   STONE D J.
TCHERNEV V T.
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  SPYTEK K A.
                                                                 TWOMLOW N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 508 AA;
                                                                                                                                   (VOSS/)
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                                                                                         (VERN/)
(ZERH/)
                                                                 (TWOM)
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Padigaru M, Patturajan M,
, Shenoy SG, Shimkets RA;
J, Tchernev VT, Twomlow N;
                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antibarkinsonian, anticonvulsant, osteopathic, antiarthritic, antinflammatory, polypeptides, nucleic acid molecules and antibodises may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular disorders including hypertension and atherosclerosis, neurodegenerative disorders each as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders asthma and dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopoiesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of
                                                                                                                                                                                             New isolated NOVX polypeptides and polynuclectides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
Miller CE, Millet I, Mishra VS, Par
Peyman JA, Rastelli L, Rieger DK, Starling G, Spytek KA, Stone DJ,
Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 54; 447pp; English.
                                                                                                                       WPI; 2003-441555/41.
                                                                                                                                              N-PSDB; ADE28676.
Mezes PS, Mi
Pena CEA, Pe
Smithson G,
                                                                        Vernet CAM,
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Sequence 508 AA;

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240 VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL 120 120 BLRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 180 180 240 300 300 360 420 SEHAQDIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS 420 AASPEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGL 480 9 9 61 VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL 121 ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 181 EVDVSAGNGAGSVORVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV 181 AVDVSAGNGAGSVQRVKILEGRIECVISNIRGRIRYTFAVRARMAEPSFGGFWSAWSEPV SLITPSDLDPLILITSLILVVILVLITVLALLSHRRALKQKIMPGIPSPESEFEGLFTTH SEHAQDIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG Gaps ö 99.1%; Score 2691; DB 7; Length 508; 99.0%; Pred. No. 1.8e-214; ive 2; Mismatches 3; Indels (Query Match
Best Local Similarity 99.0
Matches 503, Conservative 19 121 241 361 241 301 301 361 421

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Erythropoietin receptor; recombinant; murine; anaemia
                                                                                                                                                                   /note= "putative transmembrane domain"
                                                                                                                                                      /note= "mature EPO receptor"
251. .272
       481 SDGPYSNPYENSLIPAAEPLPPSYVACS 508

    .24
    /note= "signal peptide"

SDGPYSNPYENSLIPAAEPLPPSYVACS
                                                                                                                                                                                                                                      ) CHILDRENS MEDICAL CENT.
) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                             Location/Qualifiers
                                             Ş
                                          AAR47518 standard; protein; 508
                                                                                                                                                                                                                                                           Jones SS
                                                                                                                                                                                                                    89US-00306503.
                                                                                                                                                                                                        91US-00678877
                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                .508
                                                                                                                                                                                                                                                         D'andrea A, Wong GG,
                                                                                       Human EPO receptor.
                                                                                                                Homo sapiens
                                                                                                                                                                                                        25-MAR-1991;
                                                                    25-MAR-2003
24-JUN-1994
                                                                                                                                                                                                                    03-FEB-1989;
                                                                                                                                                                              US5278065-A.
                                                                                                                                                                                           11-JAN-1994
                                                        AAR47518;
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Peptide
                                                                                                                                                Protein
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(WHED )
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Recombinant DNA encoding erythropoietin receptor - used to develop prods. for study, treatment or diagnosis of disorders in which receptor is dysfunctional.

WPI; 1994-025409/03.

N-PSDB; AAQ53995

Disclosure, Fig 9; 24pp, English.

or The cDNA was used to transfer COS-1 cells and these were greened for tadioiodinated erythropoietin (EPO) binding to isolate cDNA encoding the EPO receptor. This cDNA was used as a probe to screen a human genomic cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may be used to study, treat or diagnose disorders in which the EPO receptor is dysfunctional. The EPO receptor may also be used to raise antibodied or for treating hypersensitivity to EPO or who have elevated levels of EPO. The pord, is pref. used for treating anaemias, primary proliferative polycythemia and secondary polycythemia. See also AAR47517. (Updated on 25-MAR-2003 to correct PF field.) Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library

Sequence 508 AA;

Gapa ö Length 508; 3; Indels 99.1%; Score 2690; DB 2; 98.8%; Pred. No. 2.2e-214; 3; Mismatches Conservative Similarity Query Match Best Local Simi] Matches 502; (ò

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                                                                                                                                                                                                                                KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX; antidiabetic; anorectic; cardiant; hypotensive;
antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;
                                                                                                                                 ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY
                                                                                                                 EVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                                                                                                                                     SEHAQDIYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS
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                                                                                                                                                                                                                                                                                                                                                                AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVCDSGMSTDYSSGDSQGAGGL
                                                                                                                                                                        SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH
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17-DEC-2001; 2001US-0341477P.
17-DEC-2001; 2001US-0341540P.
20-DEC-2001; 2001US-0342592P.
27-DEC-2001; 2001US-0344903P.
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2001US-0338285P.
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07-DEC-2001;
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The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, protozoacide, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, dermatological, antiasthmatic and antilipsemic activities. The anticonvulsant, osteopathic, antiarthritic, antiinflammatory, dermatological, antiasthmatic and antilipsemic activities. The color of diapetic acid molecules and antilodism may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherocolerosis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders as thma and dyslipidaemia.

Considers, inflammatory skin disorders as neurosementics may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopoiesis, wound healing and anglogenesis as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
                                                                                                                                                                                                                                                                                                              Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burges CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A; Bllerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA; Smithson G, Starling G, Spytck KA, Stone DJ, Tchernev VT, Twomlow N; Vernet CAM, Zerhusen BD, Zhong M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 52; 447pp; English.
                 15-MAY-2002; 2002US-0380981P.
17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383534P.
29-MAY-2002; 2002US-0383744P.
29-MAY-2002; 2002US-0383029P.
                                                                                                                                                                 2002US-0401788P.
2002US-0406353P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 89.2
Matches 453; Conservative
                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-441555/41.
N-PSDB; ADE28674.
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26-AUG-2002;
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ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 181 EVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV

61 VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL

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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Blerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra V, Padigaru M, Patturajan M;
Shenoy SG, Shimkets RA, Smithson G, Spaderna SK, Starling G;
Spytek KA, Stone DJ, Tchernev VT, Twomlow N, Vernet CAM;
Zerhusen BD, Vose EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human NOVX polypeptides and the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                PADIGARU M.
PENA C C B A.
PENA C C B A.
PEYRAN J A.
RASTELLI L.
RIEGER D K.
ROTHENBERG M E.
SHENOY S G.
SHIMKETS R A.
SMITHSON G.
SMITHSON G.
SPADERNA S K.
                                                                                                                                                                                                                                             MACDOUGALL J R
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KHRAMTSOV N V.
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TCHERNEV V T.
  ALVAREZ E.
ANDERSON D W.
                                                                                           ELEEMAN K.
ETTENBERG S.
GANGOLLI E A.
GERLACH V.
                                                    CASMAN S J.
CHAPOVAL A.
DHANABAL M.
                                                                                                                                                                                                                                                                  MAZUR A.
MCQUEENEY K.
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GROSSE W M.
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ZERHUSEN B D
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N-PSDB; ADM93419.
                                          BURGESS C E.
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                                                                                    EDINGER S R
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                                BOLDOG F L.
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MILLET I.
MISHRA V.
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                               (BOLD/)
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                                                                                                                   SEHAQDTYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS 420
                                                                                                                                       387
                                                                                                                                                                                                                                                                                                                                                               Human, NOVX; congenital heart defect; cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; scleroderma; adenocarcinoma; haemophilia; graft-versus-host disease; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; multiple sclerosis; diabetes; obesity; bronchial asthma; acquired immunodeficiency syndrome; AIDS; Crohn's disease;
                                                                                      KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTMQAVEPGTDDEGPLLEPVG
                                 SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKOKIWPGIPSPESEFEGLFTTH
                                                                                                                                                            AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGL
                                                                                                                                                                                                                                                                                                                                                                                                                               infectious disease; anorexia; immune disorder
                                                                                                                                SEHAQDIYLVLDKWLLPRNPPSEDLPG-----
                                                                                                                                                                                                     508
                                                                                                                                                                                                                SDGPYSSPYENSPIPAAEPLPPSYVACS 458
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                                                                                                                                                                                                                                                                               ADM93420 standard; protein; 458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001; 2001US-0330722P.

09-NOV-2001; 2001US-0330722P.

09-NOV-2001; 2001US-0335610P.

15-NOV-2001; 2001US-0335610P.

28-NOV-2001; 2001US-0333152P.

29-NOV-2001; 2001US-0333152P.

29-NOV-2001; 2001US-00997425.

29-NOV-2001; 2001US-00997425.

04-DEC-2001; 2001US-03331676P.

05-FEB-2002; 2002US-0354807P.

15-MAY-2002; 2002US-0354807P.

16-MAY-2002; 2002US-0381043P.

02-JUL-2002; 2002US-0393148P.
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06-AUG-2002; 2002US-0401626P
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2001US-0338626P
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05-NOV-2001;
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encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NoVX. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atherosclerosis, hypertension, pulmonary stenosis, scleroderma, adenocardinoma, haemophilia, graft-versus-host disease, cancer, multides and sequences. Parkinson's disease, miltides.
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                                                                                                                                                                                             multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease, anorexia and immune disorders. This sequence represents a human NOVX polypebtide of the invention. Note: The sequence data for this patent is also available from USPTO at seqdata.uspto.gov/sequence.html.
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89.2%; Pred. No. 6.1e-191;
iive 1; Mismatches 4;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         Sequence 458 AA;
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anorexia; cancer; cardiovascular; hypertension; atherosclerosis; neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune; osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; human; NOV.
  antiasthmatic; antilipaemic; metabolic; diabetes; obesity; inféctious;
                                                                                                                                                            05-NOV-2001; 2001US-0338626P.
05-DEC-2001; 2001US-0338600P.
12-DEC-2001; 2001US-0341346P.
17-DEC-2001; 2001US-0341346P.
17-DEC-2001; 2001US-0341477P.
20-DEC-2001; 2001US-0341477P.
21-DEC-2001; 2001US-034450P.
27-DEC-2001; 2001US-0344903P.
17-APR-2002; 2002US-0380981P.
15-MAY-2002; 2002US-0380981P.
17-MAY-2002; 2002US-0380981P.
18-MAY-2002; 2002US-0380981P.
28-MAY-2002; 2002US-0380981P.
28-MAY-2002; 2002US-0380981P.
28-MAY-2002; 2002US-0380981P.
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2002US-0401788P.
                                                                                                                                            05-NOV-2002; 2002WO-US035536
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31-OCT-2002; 2002US-0028731.
                                                                                                   WO2003040330-A2
                                                                                 Homo sapiens.
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07-AUG-2002;
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(CURA-) CURAGEN CORP.

Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A; Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA; Smithson G, Starling G, Spytck KA, Stone DJ, Tchernev VT, Twomlow N; Vernet CAM, Zerhusen BD, Zhong M;

N-PSDB; ADE28670.

WPI; 2003-441555/41.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections

Claim 1; SEQ ID NO 48; 447pp; English.

The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, ancrectic, cardiant, hypotensive, antiateriosclerotic, virucide, antibacterial, fungicide, protozoacide, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, anciarthritic, antiinflammatory, dermatological, antiasthmatic and antilipaemic activities. The polypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders such as Alzhelmer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders, asthma and dyslipidaemia. Furthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell WO2003040330-A2.

05-NOV-2002;

2001US-0341477P. 2001US-0341540P. 2001US-0342592P. 2001US-0344297P.

2001US-0344903P. 2002US-0373288P. 2002US-0380981P. 2002US-0381495P.

17-APR-2002; 15-MAY-2002;

17-MAY-2002;

2002US-0383534P. 2002US-0383744P. 2002US-0383829P. 2002US-0384024P. 2002US-0401788P. 2002US-0406353P

(CURA-) CURAGEN CORP.

31-OCT-2002;

WPI; 2003-441555/41.

N-PSDB; ADE28672

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Human NOV15b protein - SEQ ID 50.
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                              88.5%;
                             Query Match
Best Local Similarity 89.2°
Matches 453, Conservative
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                      Sequence 458 AA;
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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Blygess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov Nv;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Parturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
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17-DEC-2001; 2
17-DEC-2001; 2
20-DEC-2001; 2
27-DEC-2001; 2
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28-MAY-2002; 2
29-MAY-2002; 2
        differentiation and proliferation, haemopoiesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of the human NOV protein of the invention.
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                                                                                                                 Length 458;
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                                                                                                              ; Score 2404; DB 7;
; Pred. No. 1.1e-190;
.1; Mismatches 4;
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The invention relates to a novel isolated NOVX polypeptide. The cardiant, hyporensive, antiatreriosclerotic, virucide, antibacteric, cardiant, hyporensive, antiatreriosclerotic, virucide, antibacterial, cardiant, hyporensive, antiatreriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antilipace, antiparkinsonian, demnatological, antisathmatic and antilipace activities. The colypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoletic disorders, inflammatory skin disorders, asthma and dyslipidaemia.

C'Ruthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell differentiation and proliferation, haemopolesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, the human NOW yorkers of the current sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the human NOV protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; virucide; antibacterial; fungicide; protozoacide; antiarteriosclerottic; virucide; antibacterial; fungicide; protozoacide; nocoropic; neuroprotective; antiinflammatory; dermacological; antiarthritic; antiinflammatory; dermacological; antiathmatic; antilipaemic; metabolic; diabetes; obesity; infectious; anorexia; cancer; cardiovascular; hypotrension; athrosolerosis; neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune; osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; angiogenesis; gene therapy; chromosome mapping; tissue typing; human; NOV.
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Length 458;

Score 2404; DB 7; Pred. No. 1.1e-190;

88.5%;

Best Local Similarity

Query Match

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2001US-00997425
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MALYANKAR U M.
MAZUR A.
MCQUEENEY K.
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KHRAMTSOV N V.
                                                                                                                                 ALSOBROOK J P.
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ISEN A.
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GROSSE W M.
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PENNA C E A.
PEYNAN C A A.
RASTELLI L.
RIEGER D K.
ROTHENBERG M
SHENOY S G.
SHIMKETS R A
SMITHSON G.
SPADERNA S K.
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CASMAN S J.
CHAPOVAL A.
DHANABAL M.
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GANGOLLI E
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MILLER C E.
MILLET I.
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HACKETT C.
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ZERHUSEN E
VOSS E Z.
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29-NOV-2001;
29-NOV-2001;
04-DEC-2001;
05-FEB-2002;
15-MAY-2002;
16-MAY-2002;
02-JUL-2002;
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06-AUG-2002;
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07-AUG-2002;
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                                                                                           ELRVTAASGAPRYHRVIHINEVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRY 180
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                            EVDVSAGNGAGSVQRVEILEGRIFECVLSNLRGRIFRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                              SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH
                                                                                                                                                                                                                    KGNFQLWLYQNDGCLWWSACTPFTEDPPAFLEVLSERCWGTMQAVEPGTDDEGPLLEPVG
                                                                                                                                                                                                                                                                                           Human; NOVX; congenital heart defect, cardiomyopathy; atherosclerosis; hypertension; pulmonary stenosis; scleroderma; adenocarcinoma; haemophilia; graft-versus-host disease; cancer; neurodegenerative disorder; Alzheimer, s disease; Parkinson's disease; multiple sclerosis; diabetes; obesity; bronchial asthma; acquired immunodeficiency syndrome; AIDS; Crohn's disease;
                                                      VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL
                                                                                                                                EVDVSAGNGAGSVORVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPV
                                                                                                                                                                    SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKOKIWPGIPSPESEFEGLFTTH
                                                                                                                                                                                                          KGNFQLWLYQNDGCLWWSPCTPFTEDPPASLEVLSERCWGTWQAVEPGTDDEGPLLEPVG
                 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL
                                                                                                                                                                                                                                                                                  AASFEYTILDPSSQLLRPWTLCPELPPTPPHLKYLYLVVSDSGISTDYSSGDSQGAQGGL
50; Gaps
4; Indels
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1; Mismatches
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2001US-0338626P.
2001US-0333072P.
2001US-0345398P.
2001US-0348283P.
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2001US-0332152P.
2001US-0333912P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOVX polypeptide #24
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453; Conservative
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21-NOV-2001;
28-NOV-2001;
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05-NOV-2001;
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atheroselerosis, hypertension, pulmonary stenosis, scleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (ALDS), Crohn's disease, infectious disease, anorexia and immune disorders. This sequence represents a human NOVX polypeptide of the invention. Note: The sequence data for this patent is
                                                                                                                                                                                                Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
Peyman JA, Rastelli L, Rieger DK, Rothenberg ME,
Shimkets RA, Smithson G, Spaderna SK, Starling G;
Stone DJ, Tchernev VT, Twomlow N, Vernet CAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also available from USPTO at segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 48; 330pp; English
                                                                            Zhong M;
                                                                         Voss EZ,
                                                                                                                           WPI; 2004-355303/33.
N-PSDB; ADM93415.
                            Shenoy SG, Sh
Spytek KA, St
Zerhusen BD,
     Pena CEA,
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Sequence 458 AA;

4; Indels 50; Gaps Score 2404; DB 8; Length 458; Pred. No. 1.1e-190; 1; Mismatches 4; Indels 5 88.5%; 89.2%; Query Match
Best Local Similarity 89.2'
Matches 453; Conservative

VCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPL 120 9 9 MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL MDHLGASLWPQVGSLCLLLAGAAWAPPPNLPDPKFESKAALLAARGPEELLCFTERLEDL 61 ઠે 쉽 셤 ઠ

SLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRRALKQKIWPGIPSPESEFEGLFTTH 300 EVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEDV 181 241

240

EVDVSAGNGAGSVQRVEILEGRIECVLSNLRGRIRYTFAVRARMAEPSFGGFWSAWSEPV 240

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SEHAQDTYLVLDKWLLPRNPPSEDLPGPGGSVDIVAMDEGSEASSCSSALASKPSPEGAS 420

361

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458

SDGPYSNPYENSLIPAAEPLPPSYVACS 508 SDGPYSSPYENSPIPAREPLPPSYVACS

481

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431

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480

430

Search completed: April 21, 2005, 08:51:50 Job time : 191 secs

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) a Nobe : www.genoscope.cns.fr) a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                              HTC 21-JUL-2004
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AGENCOURT
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization
                                            603045374
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BX382171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     AL523633
BX406158
                                                                                                           BY710355
BX340439
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BQ919762
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BF078672
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"Corganisme"Homo sapiens"

/mol types"mRNA"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/tissue type="Placents Cot 25-normalized"

/plasmid="pCMVSPORT_6"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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CR522865.1 GI:50473672
HTC; CNSLT CDNA.
HOMC sapiens (human)
Homc sapiens
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Best Local Similarity 100.(
Matches 1527; Conservative
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Direct Submission
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
REMARK
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TITLE
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                                                                    April 20, 2005, 21:00:26 ; Search time 5262 Seconds (without alignments) 11046.017 Million cell updates/sec
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        GenCore version 5.1.6 . . Copyright (c) 1993 - 2005 Compugen Ltd.
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	CR620075 (Full-length cDNA clone CS0D1016YLOS of Placenta Cot 25-normalized of Homo sapiens (human). CR620075. CR620075. GR620075. HTC; CNSLT_CDNA. HOmo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, W. B., Gruber.C., Jessee, J. and Polayss, D. Eul.Hangth cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliangalifetech.com URL: Contact: Library was constructed Corporation 1600 Faraday Avenue Submitssion Submit	nes 1527; Conservative 0
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1 ATGGACCACCTCGGGGCGTCCCTCTGGCCCCAGGTCGGCTCCCTTTGTCTCTCTGTCGCT 60	1	

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### Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; ###################################	181 GTGTTTCTGGGAGGAGGGCGGGGGGGGCCCGGGCAACTACAGCTTCTCC 240	301 GGFGGGGTGCGCTTCTGGTGTTCGCTGCCGACACGTGGGCTTCGTGCCCCTA 360		CARGED C	619 GGCGCGCACTATCCTGACCACCTGCGGGCCGGGCTGCGCTGCGGTC 860 679 GGCCGCACCGAGTGTGTGTGTGCTGAGCCTTCGGGGCCGGGCTACCTTCGCCGTC 738 661 CGCGCGCGTATGGCTGAGCCGAGCTTCGGCGGCTTCTGGAGCGCTTGGTGGGTCGGTGGGTG	TCGCTGCTGACGCCTAGCGACCTGGACCCCTCATCCTGACGCTCTCCCTCATCCTCGTG		00TGC	961 ACCCCTTCA.CGA.GGA.CGA.CCTGCTTCCCTGGA.AGTCCTTCAGA.GGGCTGCTGGGGG 1020 1039 ACCCCTTCA.GGGA.GGA.CCTGCTTCCTGGA.AGTCCTCTCAGA.GGCTGCTGGGGG 1098 1021 ACGATGCAGCGA.GGGA.CGGGA.GGTGATGA.GGGCCCCTGCTGGGGG 1080 1101 H. C.

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
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191 910 9100 EDNY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
184 strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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1 (bases 1 to 1870)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished
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Best Local Similarity 95.3%;
Matches 1455; Conservative
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Li M. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Best Local Similarity 93.6%; Pred. No. 3.6e-311;
Matches 1527; Conservative 0; Mismatches 0;
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/clone="CSDCO03YF02"
/tissue_type="Neuroblastoma
/plasmid="pcMVSPORT_6"
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Mus musculus EPOR gene, VIRTUAL TRANSCRIPT, partial sequence,
           1025 TGCAGGCAGTGGAGCCGGGGACAGATGATGAGGGCCCCCTGCTGGAGCCAGTGGGCAGTG 1084
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When musculus (house mouse)

Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae,

I (bases I to 1452)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Reriaera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Location/Qualifiers
                                   1244 AGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCGCCCA
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                                                                                                    AGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCGGCCA
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pOMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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1124 CCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGGCCTGCGGGGACGA 1183
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83.3%; Score 1271.6; DB 3; Length 1681;
Best Local Similarity 99.7%; Pred. No. 5.9e-279;
Matches 1274; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                   /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 1082)

2. (Dases 1 to 1082)

3. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

4. Euli-length cDNA libraries and normalization

3. In May 8, 2003 this sequence version replaced gi:30449031.

3. On May 8, 2003 this sequence version replaced gi:30449031.

4. Contact: Genoscope

5. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

5. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

5. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

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6. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

7. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

8. Email: segref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

18. end enriched, double-strand cDNA was digested with Not I and cloned

19. into the Not I and Econ V sites of the pCMVSPORT 6 vector. Library

19. was normalized. Library was constructed by Life Technologies, a

19. division of Invitrogen. This sequence belongs to sequence cluster
                       CCCAGTGAGGACCTCCCAGGGCCTGGTGGCAGTGTGGACATAGTGGCCATGGATGAAGGC 1200
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BX382170 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI076YCl3 3-PRIME, mRNA sequence.
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  1021 ACGATGCAGCAGTGGAGCCGGGGACAGATGATGAGGGCCCCCTGCTGGAGCCAGTGGGC
                                                                                      AGTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCG
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI076AB07NP1&c=9443.r.
Location/Qualifiers
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/mol_type="mRNA"
/do_xref="caxon:9606"
/clone="CSODIO76YC13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." DA	Ouery Match Best Local Similarity 97.5%; Pred. No. 7.6e-212; Matches 1034; Conservative 10; Mismatches 10; Indels 7; Gaps 5;	462 GTTGGCTGACGAGGCGCCACGTACTGTTGCGCTGCCCCGCCCCGCCTGAGACCCCAT 521	522 GACGTCTCACATCCGCTACGAGGTGGACGTCTCGGCCGGC	VB GAGGGTGGAGATCCTGGAGGGCCGCACCGAGTGTGCTGAGCAACCTGCGGGGCCGGAC 641 KB H	642 GCGCTACACTTCGCCGTCCGCGCGTATGGCTGAGCCGAGCTTCGGGGGTTCTGGAG 701	702 CGCCTGGTCGGAGCCTGTGTCGCTGACGCCTAGCGACCTCGGACCCCCTCATCCTGAC 761	762 GCTCTCCCTCATCCTGGTGATCATCCTGGTGCTGCTGGCTG	822 CCGCCGGGCTTTGAAGCAGAAGATCTGGCCTGGCATCCCGAGCCGAGGCGAGTTTGA 881	882 AGGCCTCTTCACCACCACCACAGGTAACTTCCAGCTGTACCTGAATGATGATGGCTG 941	942 CCTGTGGTGGAGCCCCTGCACCGGAGGACCCACCTGCTTCCCTGGAAGTCCT 1001	1002 CTCAGAGCGCTGCTGGGGGCAGTGCAGTGCAGCGGGACAGATGATGAGGGCCC 1061	1062 CCTGCTGGAGCCAGTGGGCAGTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATG 1121	1122 GTTGCTGCCCGGAACCCGCCCAGTGAGGACCTCCCAGGGCCTGGTGGACGT 1181	1182 AGTGGCCATGGATGAAGCATCCTCCTCCTCCTTCTTGCTTTGGCCTCGAAGCC 1241	1242 CAGCCCAGAGGGACCTCTGCTGCCAGCTTTGAGTACACTATCCTGGACCCCAGCTCCCA 1301	1302 GCTCTTGCGTCCATGGACACTGTGCCCTGACCCCTACCCCACCCA	1362 CCTGTACCTTGTGGTATCTGACTCTGACTGACTACAGCTCAGGGGACTCCCA 1421
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                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (STERN), Laboratory for Genome Exploration Research Group, IRKEN Genomic Sciences Center (SSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0065, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
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Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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GB|NM_010149, evidence: BLASTN, 99%, match=1523)
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/mol type="mRNA"
/dstain="GSTBL/GJ"
/db xref="FANTOM DB:2510015H03"
/db xref="taxon:10090"
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS00M009V02"
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/dev_stage="fetal"
/clone lib="Homo sapiens FETAL LIVER"
/note=Torgan: liver; Vector: pCMVSPORT 6; lst strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV slites of the pCMVSPORT 6
vector. Library was not normalized."
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NortI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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1. (Dases 1 to 984)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
   605 GGCCATGGAAGGCTCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAG
                                                                                                            1185 GGCCATGGATGAAGGCTCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAG
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This sequence belongs to sequence cluster, 9443.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSOAW009BB11QP1&c=9443.r.

Location/Qualifiers
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Contact: Genoscope
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1320)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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EST 30-MAR-2004

AL553257
AL553257 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA

RESULT 12 ALS53257 LOCUS DEFINITION

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13. (bases 1 to 1079)
14. (bases 1 to 1079)
15. Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
16. Full-length cDNA libraries and normalization
17. On Feb 15. 2011 this sequence version replaced gi:31275071.
18. Contact: Genoscope
18. Centre National de Sequencage
18. The Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
18. Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr
18. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-gerrand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/note="ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and scor v
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1079)
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http://www.genoscope.cns.fr/cdna?s=CSODI073DH11QP1&c=9443.r.
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   mRNA sequence
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/clone="CS0DI073YP22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
clone CS0DI073YP22 5-PRIME,
                                                          GI:45858026
                                                                                                                         sapiens (human)
                                                                                                                                                          Homo sapiens
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AL553257.3
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	Query Match 53.2%; Score 812.2; DB 5; Length 1005; Best Local Similarity 96.1%; Pred. No. 2.7e-174; Matches 864; Conservative 18; Mismatches 12; Indels 5; Gaps 5;	1	61 GGGGCGCCTGGGGGCCCCGGCTAACCTCCGGGACCCCAAGTTCGAGAGCGGCC 12 153 GGGCCGCCTGGGCGCCCCCGCCTAACCTCCGGACCCCAAGTTCGAGAGCGGCC 21	Qy 121 TTGCTGGCGCCCCGGGGGCCCCGAAGAGCTTCTGTGCTTCACCGAGCGGTTGGAAGACTTG 180 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 181 GIGIGITICIGGAGAGAGCGGCGGGCGGGGGGCCCGGGCAACTACAGCTICICC 240		Oy 301 GGTGGGTGCGTTCTGGTGTTCGCTGCCTACGCCGACGTCGAGCTTCGTGCCCTA 360	OY 361 GAGTTGCGCGTCACAGCAGCCTCCGGGGTATCACCGTGTCACTCAAT 420	0y 421 GAAGTAGTCCTAGACGCCCCCGTGGGGGTGGTGGCGCGGTTGGCTGACGAGAGGGG 480	OY 481 CACGTAGTGGCTGCCGCCGCCGCGCCCAGACCCCATGACGTCTCACATCCGCTAC 540	Oy 541 GAGGTGGACGTCTCGGCGAACGGCAACGGGGGGGGGGGG	Oy 601 GGCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCCGGACCGCTACACCTTCGCCGTC 660 1 1 1 1 1 1 1 1 1	0y 661 CGCGCGCGTATGGCTGAGCCGAGCTTCGGCGCCTTCTGGAGCGCCTGGTCGGAGCCTGTG 720	9y 721 TCGCTGCTGACGCCTAGCGACCTCGACCCCTCATCCTGACGCTCTCCTCGTG 780	Oy 781 GTCATCCTGGTGCTGCTGGTCGCGCTGCTCCCACCGCCGGCTCTGAAGCAG 840	OY 841 AAGATCTGGCCTGGCATCCCGAGCCCAGAGAGCGACTTTGAAGGCCTCTTCACCACCCA 899	RESULT 14 BX448343/c LOCUS BX448343 1051 bp mRNA linear EST 05-MAY-2004
Db 463 GAAGTAGTGCTCCMAGACGCCCCGTGGGGCTNGGTGGCGGGTTGGCTGACGAGGCGG 522 Qy 480 CCACGTAGTGTTGCGCTGGCTCCGCCGCCTGAGACACCCATGACGTCTCACATCCGCTA 539	523 CCANGINGAGICIGGGCIGGGICCCGCCCGACCCCACCCC	QY 600 GGGCCGCACCGAGTGTGTGCTGAACCTGCGGGGCCGGACGCGTTCGCCGT 659 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 660 CCGCGCGCGTATGGCTGAGCTTCGGCGGCTTCTGGAGCGCCTGGTCGAGCCTGT 719 Db 703 CCGCGCGCGTATGGCTGAGCTTCGGCGGCTTCTGGAGCCTCGTGGAGCCTGT 762	Oy 720 GTGGCTGAGGGACCTGGACCCCTCATCCTGACGCTCTCCCTCATCCTGGT 779	GAAGCA GAAGCA	Qy 840 GAAGATCTGGCCTGGCATCCCGAGCCCAAGAGCGAGTTTGAAGGCCTCTTCACCACCCA 899 Db 883 GAAGATCTGGCCTGGCATCYCGAGCCCCAGAAGCGAGTTKAAAGGCTCTTCACAAACA 940	OY 900 CAAGGGTAACTTCCAGCTGTGGCTGTCAGAATGATGGCTGC 942	RESULT 13	DESTRUCTION BX335579 1005 bp mRNA linear EST 08-APR-2004 DEFINITION BX335579 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA C10ne CS0DI016YL05 5-PRIME, mRNA sequence.	VERSION BX33579.2 GI:46281994 KEYWORDS EST. SOURCE Homo eapleins (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE I (bases I to 1005)	TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT ON May 2, 2003 this sequence version replaced gi:30345434.	Contact: dendscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr		division of invillogen. Ints sequence delongs to sequence cluster 9443.r. For more information about this cluster, see http://www.genoscope.ons.fr/cdna?s=CSODIO16CF03QP1&c=9443.r. Frammer	rce.	/db_xref="taxon:9606" /clone="CSODIO16YLOS" /tissue type="PLACENTA COT 25-NORWALIZED" /clone=lib="Homo sapiens PLACENTA COT 25-NORWALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT)

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1228
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                                                                                                                                                                                                                                                                                                                                                                                                                               326
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Pan troglodytes BPOR gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (Dases 1 to 1115)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G.; Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, W. A., Inderring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                      565 GCAGTGTGGACATAGTGGCCATGGATGAAGGCTCAGAAGCATCCTCCTCCTGCTTTGCTT
                                                                                                                                                                                                                                    505 TGGCCTCGAAGCCCAGCCCAGAGGAGCCTCTGCTGCCAGCTTTGAGTACACTATCCTGG
                                                                                                                                                                                                                                                                                                                            445 ACCCCAGCTCCCAGCTCTTGCGTCCATGGACACTGTGCCCTGAGCTGCCCCCTACCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                 385 CCCACCTAAAGTACCTGTACCTTGTGGTATCTGACTCTGGCATCTCAACTGACTTACAGCT
                                       TGCTGGACAAATGGTTGCTGCCCCGGAACCCGCCCAGTGAGGACCTCCCAGGGCCTGGTG
                                                              1229 TGGCCTCGAAGCCCCAGAGGCGCAGAGGCTCTGCTGCCAGCTTTGAGTACACTATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                        1349 CCCACCTAAAGTACCTGTACCTTGTGGTATCTGACTCTGGCATCTCAACTGACTACAGCT
                                                                                                                        1169 GCAGTGTGGACATAGTGGCCATGGATGAAGGCTCAGAAGCATCCTCCTCCTCATGCTT
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Pred. No. 5.4e-169;
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM5360"
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Location/Qualifiers
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AY414847.1 GI:39770806
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71.0%;
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Best Local Similarity
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                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1051)

Euli, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

In Unpublished (2001)

On May 22, 2003 this sequence version replaced gi:31019923.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRY sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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/dev stage="fetal"
/clone_lib="Homo septens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division of Invitrogen.
This sequence cluster 9443.r
For more information about this cluster, see
http://www.genoscope.ons.fr/cdna?s=CSOAM009BB11NP1&c=9443.r.
Location/Qualifiers
BX448343 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODMO09YC22 3-PRIME, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM009YC22"
                                                                                BX448343.2 GI:47052187
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Aag53994 MEL EPO r	Aaq44854 Mouse sol		Abz83469 Toxicolog	Adr70427 Vector pA	Adr70421 Vector pA	Aal41116 Plasmid p			Aal41115 Plasmid p	Abz23425 Nucleotid	Adr70403 Vector pA	Abz23429 Nucleotid	Adr70409 Vector pA	Nucleoti	Aal41114 Plasmid p	Abz23428 Nucleotid	Adr70415 Vector pA	Aat48800 Plasmid m	Aav04434 Erythropo	4	m	Aal43171 Human exp	Aax58148 CadC-fusi	Abq73377 Vector pR
AAQ53994	AAQ44854	AAQ81891	ABZ83469	ADR70427	ADR70421	AAL41116	ABN84078	AAL41112	AAL41115	ABZ23425	ADR70403	ABZ23429	ADR70409	ABZ23424	AAL41114	ABZ23428	ADR70415	AAT48800	AAV04434	AAZ30854	AAL43173	AAL43171	AAX58148	ABQ73377
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1075.8	1075.8	1075.8	1024	811.2	811.2	810.4	810.4	810.4	810.4	810	810	9.608	9.608	809.2	808.8	808	808	750.4	750	750	748.2	741	700.4	602.8
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ALIGNMENTS

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Erythropoietin receptor; extracellular domain; plasmid pJYL26; ds.
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//tag= d
//note= "extracellular domain"
73..87
/ttag= b
/note= "forward primer AAQ82991 site"
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25. 250
/*tag= c
note= "extracellular domain"
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1. .1527
                                                                                                            Human erythropoietin receptor cDNA.
AAQ82990 standard; cDNA; 1527.BP
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                                                            (revised)
(first entry)
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P-PSDB; AAR70032.
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                                                           25-MAR-2003
07-OCT-1995
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                                                                                                                     AAGATCTGGCCTGGCATCCCGAGGCCCAGAGCGAGTTTGAAGGCCTCTTCACCACCAC
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                                                                The cDNA encodes human full-length erythropoietin receptor (EPO-R). Primers AAQ82991 and AAQ82992 are used to isolate fragments (nr. 73-750 and 25-250) representing the extracellular domain of the receptor. The fragments are cloned in vector plasmid pGEX-77, resulting in vector pJYL26, which encodes the extracellular domain as a fusion protein with glutathione-S-transferase. The extracellular domain of EPO-R is used for investigating the structure of the EPO-R and for identifying factors involved in regulating differentiation and proliferation mechanisms in erythroid progenitor cells. It can also be used for identifying and quantitating EPO and EPO-R as well as in understanding haematopoietic malignancy and some cardiovascular system disorders. (Updated on 25-WAR-2003 to correct PN field.)
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 human erythropoietin receptor fragment - obtd. by expression protein having a thrombin proteolytic cleavage site.
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        18-OCT-2002; 2002US-0418988P
            GENENTECH INC.
WU T D.
ZHOU Y.
                         WPI; 2004-534300/51
                     Zhou Y;
22-JUL-2004
            (GETH ) (
                (ZHOU/)
                    Wu TD,
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID No:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% composed identity to (a)-(c); or (b) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above comprising the above expression vector; (a) a process for producing a polypeptide; (4) an isolated polypeptide comprising the above polypeptide (b) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide (c) an isolated antibody that binds to the above polypeptide; (f) a process of the above polypeptide fused to a heterologous polypeptide; (f) an isolated oligopeptide; (g) a tumour-associated antigenic target (TAT) binding organic molecule; (g) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (l) a composition of matter comprising the above polypeptide; (l) a numbody, oligopeptide or TAT binding organic molecule; in combination where the growth of the cell is at least in part dependent upon a growth contributing the growth of a cell that expresses the above protein; (l) a method of determining the provent of the above protein; (l) a method of containing the prosence of a tumour comprising cherapeutically treating a mammal having a cancerous tumour comprising character and described above; (l5) methods of diagnosing the presence of a tumour in a mammal; (l6) a method for treating or preventing a cell proliferative or contained with interested expression or activity of the above protein; (l6) and contained with interested expression or activity of the above protein; (l6) and contained with interesting or preventing or activity of the above protein; (preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer human TAT cDNA sequence from the present invention. Claim 1; SEQ ID NO 360; 5504pp; English.

Sequence 1848 BP; 313 A; 593 C; 577 G; 365 T; 0 U; 0 Other;

1021 1157 1081 1217 1141 1277 1201 ò а ò 셤 à 셤 ò ö 256 121 TTGCTGGCGCCCCGGGGCCCCGAAGAGCTTCTGTGCTTCACCGAGCGGTTGGAGGACTTG 180 61 GGGGCCGCCTGGGCGCCCCGCCTAACCTCCCGGACCCCCAAGTTCGAGAGCAAAGCGGCC 120 137 Aredaccaccricedescercereresceceaserescricerritererecreeres 9 197 GGGGCCGCCTGGGGCGCCCCCGCCTAACCTCCCGGACCCCAAGTTCGAGAGCAAAGCGGCC 1 ATGGACCACCTCGGGGCGTCCCTCTGGCCCCAGGTCGGCTCCCTTTGTCTCCTGCTCGCT Gaps 100.0%; Score 1527; DB.13; Length 1848; 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.0%;
Matches 1527; Conservative 0 ઠે a ઠે

1216 1140 1260 AGTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCC 1276 ACCCCTTCACGGAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAGGCGCTGCTGGGGG 1020 257 TTGCTGGCGGCCCCGGGGGCCCCGAAGAGCTTCTGTGCTTCACCCAGCGGTTGGAGGACGACTTG 316 241 TACCAGCTCGAGGATGAGCCATGGAAGCTGTGTCGCCTGCACCAGGCTCCCACGGCTCGT 300 840 900 496 420 480 616 540 919 900 736 999 796 720 856 780 916 317 GTGTGTTTCTGGGAGGAGGGGGGGGGGGGGGGGCCCGGGCAACTACAGCTTCTCCC 437 GGTGCGGTGCGCTTCTGGTGTTCGCTACAGCCGACACGTCGAGCTTCGTGCCCCTA 677 GAGGTGGACGTCTCGGCCGGCAACGGCGCAGGAGCGTACAGAGGGTGGAGAGTCCTGGAG GGCCGCACCGAGTGTGTGTGTGAGCAACCTGCGGGCCGGACGCGCTACACCTTCGCCGTC 857 reserisereacie crascia de conservencia de contra de GTCATCCTGGTGCTGACCGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAGCAG GTGTGTTTCTGGGAGGAAGCGGCGAGCGCTGGGGTGGGCCCCGGGCAACTACAGCTTCTCC 377 TACCAGCTCGAGGATGAGCCATGGAAGCTGTGTGTCGCCTGCACGGCTCCCACGGCTCGT 557 GAAGTAGTGCTCCTAGACGCCCCCGTGGGGCTGGTGGCGCGCTTGGCTGACGAGAGCGGC 617 CACGTAGTGTTGCGCTGGCTCCCGCCTGAGACACCCATGACGTCTCACATCCGCTAC GAGGTGGACGTCTCGGCCGGCAACGGCGCAGGGAGCGTACAGAGGGTGGAGATCCTGGAG GCCGCACCGAGTGTGTGTGTGAGCAACCTGCGGGGCCGGACGCGCTACACCTTCGCCGTC CCCCCCCTATGCCTGAGCCCGAGCTTCGGCGGCTTCTGGAGCGCCTGGTCGGAGCCTGTG TCGCTGCTGACGCCTAGCGACCTGGACCCCTCATCCTGACGCTCTCCCTCATCCTCGTG 301.GGTGCGGTGCGCTTCTGGTGTTTCGCTGCCTACAGCCGACACGTCGAGCTTCGTGCCCCTA 497 GAGTTGCGCGTCACAGCAGCCTCCGGCGCTCCGCGATATCACCGTGTCATCCACAAT CGCGCGCGTATGGCTGAGCCGGCTTCGGCGCGTCTGGAGCGCCTGGTCGGAGCCTGTG GAGTTGCGCGTCACAGCAGCCTCCGGCGCTCCGGCGATATCACCGTGTCATCCACATCAAT CACGTAGTGTTGCGCTGGCTCCCGCCCTGAGACACCCCATGACGTCTCACATCCGCTAC AAGGGTAACTITCCAGCTGTGGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCCCCTGC ACGATGCAGGCAGTGGAGCCGGGGACAGATGAGGGCCCCCCTGCTGGAGCCAGTGGGC AGTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCCGGAACCCCG TCAGAAGCATCCTCCTCTCATCTGCTTTGGCCTCGAAGCCCAGCCCAGAGGGAGCCTCT CCCAGTGAGGACCTCCCAGGGCCTGGTGGCAGTGTGGACATAGTGGCCATGGATGAAGGC 1037 181 361 421 481 541 601 737 661 797 721 781 917 841 901 196 1097 ઠે ò 셤 ò 셤 g ઠે 셤 ઠે õ d ò පු ò 셤 ò ద à g ò g ò ద ò 셤 ò 엄

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benefits from modulating the balance of regulatory T cell function relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGBR2 and TGFbetal, or Jaggad-1, GRR-32, CDB3, CDB4, CDB9, serotonin R, BYS5, serotonin R2C, GPR63, histamine R-H4, GPR59, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-srelated kinase to the subject, such that treatmen occurs. The methods are useful for diagnosing, preventing or treating conditions characterized by a too-vigorous or weak effector T cell or regulatory T cell response to antigens associated with the condition, such as in an allergic response, an autoimmune disorder, a viral infection, such as in an infection, a parasatic infection or a tumour. The present sequence represents a DNA encoding a human erythropoietin receptor (BPOR), preferentially expressed in regulatory T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGCGGTGCGTTTTCGCTGCTTACAGCCGACACGTCGAGCTTCGTGCCCCTA 360
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                                                                                                                                                                                                                                                                                                                                                                    1517 GACTCTGGCATCTCAACTGACTACAGCTCCAGGGACTCCCAGGGAGCCCAAGGGGGGCTTA
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                   TCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAGCCCCAGGGGAGGCCTCT
                                                                       GCTGCCAGCTTTGAGTACACTATCCTGGACCCCCAGCTCCCAGCTCTTGCGTCCATGGACA
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                                                                                                                                         GCTGCCAGCTTTGAGTACACTATCCTGGACCCCCAGCTCCCAGCTCTTGCGTCCATGGACA
                                                                                                                                                                                                    CTGTGCCCTGAGCTGCCCCCTACCCCACCCCAAAGTACCTGTACCTTGTGGGTATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; gene; ds; erythropoietin receptor; EPOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "erythropoietin receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human erythropoietin receptor (EPOR) encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCCCAGCTATGTGGCTTGCTCTTAG 1527
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137. .1663
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09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
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Morris M;

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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic felct, lung, bone marrow or stem cell transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic and vanotransplant rejection or method or seem cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The method are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a many reference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
                                                                                                                                                              Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT polypeptide; during proteins comprising a TAT polypeptide; during proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antisgonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression particularly cancers such as breast cancer, cancer, parceral cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, cancer, 
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                                                                                                                                                                                                                                                                                                        Tumour-associated antigenic target (TAT) cDNA DNA218271, SEQ ID NO:5258.
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                                                                                                                                                                                                                                                                                                                                                                                                      Tumour-associated antigenic target; TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bandder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
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useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
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ACN40465 standard; cDNA; 1849 BP.
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erythropoietin receptor extracellular domain; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human erythropoietin receptor encoding cDNA SEQ ID NO:4.
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    cythemia vera. See also AAQ05747 (murine EPO receptor clone). (Updated
on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
PI field.)

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100.0%; Score 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches
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                                                                                                                                                                                                                  The present invention describes a purified human erythropoietin. (BPO)

receptor polypeptide, which consists essentially of amino acids 25-250 of

the full length human BPO receptor protein. The human BPO receptor

polypeptide sapement having an amino terminus and a carboxyl terminus, the

segment having a manio terminus and a carboxyl terminus, the

cepment having a thrombin proteolytic cleavage site at the carboxyl

terminus; and (b) a second polypeptide segment consisting essentially of

the purified human BPO receptor, where the second polypeptide segment is

covalently coupled to the carboxyl terminus of the first polypeptide

segment. The human BPO receptor polypeptide is useful for studying ligand

segment. The bumpan BPO receptor polypeptide is useful for studying ligand

covalently coupled is also useful for amalysing and understanding

receptor. The polypeptide is also useful for analysing and understanding

receptor structure and signal transduction. The present sequence encodes

human BPO receptor from the present invention
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                                                                                               New purified human erythropoietin receptor polypeptide, useful for studying ligand binding to erythropoietin receptor, as well as for analyzing and understanding receptor structure and signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1527 BP; 246 A; 514 C; 469 G; 298 T; 0 U; 0 Other;
                                                                                                                                                                                    Example 1; Page 9-10; 19pp; English
                                  WPI; 2002-361181/39.
P-PSDB; ABB09173.
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                                     Erythropoietin receptor; cDNA; anemia therapy; diagnostic;
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Pred. No. 0;
0; Mismatches
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 Human erythropoietin receptor cDNA
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Best Local Similarity 99.9%;
Matches 1526; Conservative
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                                                                                                                                  GCTGCCAGCTTTGAGTACACTATCCTGGACCCCAGCTCCCAGCTCTTGCGTCCATGGACA
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CCCAGTGAGGACCTCCCAGGGCCTGGTGGCAGTGTGGACATAGTGGCCATGGATGAAGGC
                 1246 CCCAGTGAGGACCTCCCAGGCCTGGTGGAGACATAGTGGCCATGGATGAAGGC
                                                                              TCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAGGCGCAGAGGGAGCCTCT
                                                                                                                  GCTGCCAGCTTTGAGTACACTATCCTGGACCCCCAGCTCCCAGCTCTTGCGTCCATGGACA
                                                                                                                                                                                                                                     GACTCTGGCATCTCAACTGACTACAGCTCAGGGGACTCCCAGGGGGGGCCTTA
                                                       TCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAGGCCAGAGGGAAGCCTCT
                                                                                                                                                                          CTGTGCCCTGAGCTGCCCCTACCCCACCCAACCTAAAGTACCTGTACCTTGTGGTATCT
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2001US-0338285P.
2001US-0341346P.
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2001US-0341540P.
2001US-0342592P.
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05-DEC-2001;
07-DEC-2001;
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17-DEC-2001;
17-DEC-2001;
20-DEC-2001;
31-DEC-2001;
17-APR-2002;
15-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2002;
28-MAY-2002;
28-MAY-2002;
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The invention relates to a novel isolated NOVX polypeptide. The cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, tungicide, protozoacide, nootropic, neuroprotective, antiparkingonian, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, cardiocopathic, antiarthritic, antiinflammatory, anticonvulsant, osteopathic, infections and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obsisty, infections diseases, ancrexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders, asthma and dyslipidaemia.

Furthermore, the nucleic acids and polypeptides may also be used to disease and epiles may also be used to differentiation and proliferation, haempoiesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hypotidisation probes, in chromosome mapping, tissue typing, the human NOV CDNA of the invention.
                                                                                                                                                                        Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Gasman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Marses PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGGGCGCCTGGGCGCCCCCGCCTAACCTCCCGGACCCCCAAGTTCGAGAGCAAAGCGGGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TIGCIGGCCCCGGGGCCCCGAAGAGCTICTGTGCTICACCGAGCGGTTGGAGGACTIG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 ATGGACCACCTCGGGGGGGTCCCTCTGGCCCCAGGTCGGCTCCCTTTTGTCTCCTGCCCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 TTGCTGGCGGCCCGGGGGCCCGAAGAGCTTCTGTGCTTCACCGAGCGGTTGGAGGACTTG
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 53; 447pp; English.
                       29-MAY-2002; 2002US-0384024P.
07-AUG-2002; 2002US-0401788P.
26-AUG-2002; 2002US-04065559
31-OCT-2002; 2002US-002857971.
  2002US-0383829P
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Matches 1523; Conservative
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                                                                                                                                  (CURA-) CURAGEN CORP
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                          GACTCTGGCATCTCAACTGACTTACAGCTCAGGGGACTCCCAGGGGAGCCCAAGGGGGGCTTA
                                                  GACTCTGGCATCTCAACTGACTACAGGGGACTCCCAGGGAGCCCAAGGGGGGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; NOVX; gene; ss; congenital heart defect; cardiomyopathy;
                                                                                                                                                                                                                             CCCCCCAGCTATGTGGCTTGCTCTTAG 1538
                                                                                                                                                                                                        CCCCCCAGCTATGTGCCTTGCTCTTAG 1527
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06-NOV-2001; 2001US-0338626P.
06-NOV-2001; 2001US-0345398P.
09-NOV-2001; 2001US-0345398P.
15-NOV-2001; 2001US-0345398P.
21-NOV-2001; 2001US-0335610P.
21-NOV-2001; 2001US-0333912P.
28-NOV-2001; 2001US-0333912P.
29-NOV-2001; 2001US-0334300P.
04-DEC-2001; 2001US-0334300P.
04-DEC-2001; 2001US-033480P.
15-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-0381086P.
16-MAY-2002; 2002US-038108P.
02-JUL-2002; 2002US-038108P.
06-AUG-2002; 2002US-0401526P.
06-AUG-2002; 2002US-0401539P.
26-AUG-2002; 2002US-0401539P.
                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA; 1585
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BOLDOG F L.
BURGESS C E.
CASMAN S J.
CHAPOVAL A.
BDHANBAL M.
EDINGER S R.
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 multiple sclerosis, diabetes, obesity, bronchial asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, infectious disease, anotexia and immune discorders. This submance represents a human NOVX polymucleotide of the invention. Note: The sequence data for this patent is also available from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                               GGGGCCCCTGGGCCCCCCCCCCTAACCTCCCGGACCCCAAGTTCGAGAGCGGCC
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                                                                                                                          DB 12; Length 1585;
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                                                                                            Sequence 1585 BP; 263 A; 531 C; 486 G; 305 T; 0 U; 0 Other;
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                                                                                                                       Score 1520.6;
Pred. No. 0;
0; Mismatches
                                                                                                                       Query Match
Best Local Similarity 99.7%;
Matches 1523; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The NOVX polypeptides and polynucleotides are useful for determining the presence of or predisposition to a disease associated with altered levels of the sequences in a mammalian subject, and for treating or preventing a pathology associated with NOVX. The polypeptides, polynucleotides and antibodies that bind immunospecifically to the polypeptides are useful for treating or preventing disorders or syndromes such as congenital heart defects, cardiomyopathy, atherosate and archeroselerosis, hypertension, pulmonary stenosis, scleroderma, adenocarcinoma, haemophilia, graft-versus-host disease, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach V, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mequeeney K;
Mezes PS, Miller CE, Millet I, Mishra V, Padigaru M, Patturajan M;
Shenoy SG, Shimkete RA, Smithson G, Spaderna SK, Starling G;
Spytek KA, Stone DJ, Tcherav VT, Twomlow N, Vernet CAM;
Zerhusen BD, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, diabetes, obesity, cancer, bronchial asthma, Crohn's disease.
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ROTHENBERG M E.
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SHIMKETS R A.
SMITHSON G.
SPADERNA S K.
STARLING G.
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KHRAMTSOV N V.
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PEYMAN J A.
RASTELLI L.
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VERNET C A M.
ZERHUSEN B D.
VOSS E Z.
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MCZES P.S.
MILLER C.B.
MILLET I.
MISHRA V.
PADIGARU M.
ELLERMAN K.
ETTENBERG S.
GANGOLLI E A
GERLACH V.
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TCHERNEV V T.
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HACKETT C.
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(ETTE/)
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Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library. The cDNA was used to transfect COS-1 cells and these were screened for radioiodinated erythropoietin (EPO) binding to isolate cDNA encoding the EPO receptor. This cDNA was used as a probe to screen a human genomic cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may be used to study, treat or diagnose disorders in which the EPO receptor is dysfunctional. See also AAQ53994. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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Pred. No. 0;
0; Mismatches
               (GEMY ) GENETICS INST INC.
(CHIL-) CHILDRENS MEDICAL CENT.
(WHED ) WHITEHEAD INST BIOMEDICAL
                                                                           Jones SS
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Matches 1520; Conservative
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(first entry)
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Truncated human EpoR; erythropoietin receptor; hypersensitive EpoR(t439); mutant human EpoR; EpoR signalling; cancer; infectious disease; HIV; sickle cell anaemia; cytostatic; antimicrobial; antiviral; immunostimulant; anti-anaemic; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present cDNA sequence encodes truncated human EpoR (erythropoietin receptor). This was isolated from human umblical cord blood LDNMC using standard PCR methods. Transfection of constitutively active EpoR(t413) by electroporation into a cytokine-dependent cell line supports cell population expansion in the absence of exogenous cytokines. Mutant human EpoR is used in treatment of disorders related to inadequate EpoR signalling. The transfected cells may also used in gene therapy to treat cancer, infectious diseases (e.g. HIV), sickle cell anaemia, and conditions related to abnormal expression of erythropoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.9%; Score 1312.2; DB 3; Length 99.8%; Pred. No. 2.3e-272; ive 0; Mismatches 3; Indels
                                                                                                                                              "Truncated human EpoR(t439)"
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Mueller SG;
                                                                                                                                                                                                                                                                                                                                                                                                                          used for production of hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Fig 9; 61pp; English.
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Matches 1314; Conservative
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                                                                                                                                                                                                                                                                                                        (HEMO-) HEMOSOL INC.
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(first entry)

07-APR-2000

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Truncated human EpoR; erythropoietin receptor; mutant human EpoR;
EpoR signalling; cancer; infectious disease; HIV; sickle cell anaemia;
cytostatic; antimicrobial; antiviral; immunostimulant; anti-anaemic; ss
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85.6%; Score 1307.4; DB 3;
Best Local Similarity 99.5%; Pred. No. 2.4e-271;
Matches 1311; Conservative 0; Mismatches 6;
                                                                                                                                                                                                         "R154C human EpoR(t439)"
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NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiathritic; antiinflammacory; dermatological; antiathritic; antiinflammacory; dermatological; anorexia; cancer; cardiovascular; hypertension; atherosclarosis; neurodegenerative; Alzhaimer's disease; Parkinson's; epilopsy; immune; osteoarthritis; haemopoietic; inflammacory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopoiesis; wound healing; anglogenesis; gene therapy; chromosome mapping; tissue typing; human; ss; gene; NOV.
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05-DEC-2001; 2001US-0336600P.
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29-MAY-2002; 2002US-0383539P.
26-AUG-2002; 2002US-0401788P.
26-AUG-2002; 2002US-0401788P.
                                                                        Human NOV15a cDNA - SEQ ID 47.
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(first entry).
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   29-JAN-2004
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(CURA-) CURAGEN CORP.

Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;
Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Bilerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
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Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytck KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;

WPI; 2003-441555/41. P-PSDB; ADE28671.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

Claim 20; SEQ ID NO 47; 447pp; English.

The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonlan, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, dermatological, antiasthmatic and antilipaemic activities. The polypeptides, nucleic acid molecules and antibodies may be useful for

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2001US-0338285P.
2001US-0341346P.
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2001US-0342592P.
2001US-0344297P.
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2002US-00287971.
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Homo sapiens.
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UM, Mazur A, Mcqueeney K;
Padigaru M, Patturajan M;
Shenoy SG, Shimkets RA;
J, Tchernev VT, Twomlow N; Eisen A; Gorman L; Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Bllerman K, Ettenberg S, Gangolli EA, Gerlach VI, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV, Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcges PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patt Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shi Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Vernet CAM, Zerhusen BD, Zhong M;

WPI; 2003-441555/41. P-PSDB; ADE28673.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

Claim 20; SEQ ID NO 49; 447pp; English

The invention relates to a novel isolated NOVX polypeptide. The CC cardiant, hypotensive, antiartes, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, protozoacide, noctropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antiarilammatory.

Cc dermatological, antiasthmatic and antilipaemic activities. The cc polypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and adisease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders, asthma and dyslipidaemia.

Cc disorders, inflammatory skin disorders, asthma and dyslipidaemia.

Cc disorders, inclammatory skin disorders, asthma and dyslipidaemia.

Cc disorders, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, be used as hybridisation probes, in chromosome mapping, tissue typing, creventive medicine and pharmacogenomics. The current sequence is that of the human NOV cDNA of the invention.

Sequence 1733 BP; 291 A; 558 C; 546 G; 338 T; 0 U; 0 Other;

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: April 20, 2005, 19:31:21; Search time 6669 Seconds (without alignments) 11094.784 Million cell updates/sec	e: table: d: DB seq l	GenEmbl:* 1. gb_ba:* 2. gb_htg:* 3. gb_htg:* 4. gb_om:* 5. gb_ov:* 6. gb_pat:* 7. gb_ph:* 8. gb_pl:* 11: gb_sts:* 11: gb_sts:* 11: gb_sts:* 11: gb_sts:* 14: gb_vi:*	### Score Action 1987 of the total score distribution. #### Score Match Length DB ID Score Match Length DB ID Score Match L	1307.4 85.6 1317 6 AR202362 ARX020362 Sequence 1307.4 85.6 1317 6 ARX09201 AXX008201 Sequence 1207.6 83.6 1314 9 BC019092 BC019092 Homo sapi 12176.6 83.6 5761 9 AK074082 AK774082 Homo sapi 11276.6 83.6 1341 10 BC019092 AK774082 Homo sapi 1185.6 75.7 1843 4 AF274305 AX774082 Homo sapi 1080.6 70.8 1741 10 BC01993 BC019993 B

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Methods for identification of cancer cell surface moleculators specific promoters, and therapeutic uses thereof Patent: WO 03000928-A 191 03-JAN-2003;
Odin Medical A/S (DK)

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AVRARMAEPSFGGFWSAWSEPVSLLTPSDLDPLILTLSLILVVILVLLTVLALLSHRR
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                                                                                                                                                                                                                             Length 1624;
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llarity 100.0%; Pred. No. 1.5e-257;
Conservative 0; Mismatches 0;
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erythropoietin receptor.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1818)
Jones, S.S., D'Andrea, A.D., Haines, L.L. and Wong, G.G.
Human erythropoietin receptor: cloning, expression, and biologic
                                      1126 ACGATGCAGGCAGTGGAGCCGGGGACAGATGATGAGGCCCCCCTGCTGGAGCCAGTGGGC
                                                                                                                                                                  CCCAGTGAGGACCTCCCAGGGCCTGGTGGCAGTGGGACATAGTGGCCATGGATGAAGGC
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| db_type="mRNA"
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| 1818
| 1818
| 1612
| 1623
| gene="EPOR"
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Blood 76 (1), 31-35 (1990)
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                             Length 1818;
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                             Query Match 100.0%; Score 1527; DB 6; Best Local Similarity 100.0%; Pred. No. 1.5e-257; Matches 1527; Conservative 0; Mismatches 0;
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      GTCATCCTGGTGCTGACCGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAGCAG
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Location/Qualifiers
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1201 TCAGAAGCATCCTCGTCATCTGGCCTCGAAGCCCAGCCC	AR202361 1317 bp DNA linear Sequence 4 from patent US 6361998. AR202361 AR202361.1 GI:20256900 Unknown. Unknown. Unclassified. Unclassified. 1 (bases 1 to 1317) 1 (bases 1 to 1317) Patent: US 6361998-A 4 26-MAR-2002; Location/Qualifiers 1131131131131131131	Query Match 85.9\$; Score 1312.2; DB 6; Length 1317; Best Local Similarity 99.8\$; Pred. No. 6.38-220; 0; Gaps 0; Matches 1314; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 0; Mismatches 3; Indels 0; Gaps 0; QY 1 ArGGACCACTCGGGGCGTCCCTTGGCCCCAGGTCGCTCCTTTGTCTCCTGCTGCT 60 Db 1 ArGGACCACTCGGGGCGTCCCTTGGCCCCAGGTCGGTCCCTTTGTCTCTGCTGCT 60 QY 61 GGGGCGCTGGGGGCCCCGGCTCAACTTCGGACCCCAAGTTCGAGGCAAAGCGGC 120 Db 61 GGGGCGCCTGGGGCCCCGAAGCTTTTGTCTTCTCTTGTTCTCTTGTTCTTCTTGTTGTTG
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The efficient culture of stem cells for the hemoglobin Patent: WO 9967360-A 4 29-DEC-1999;
HEMOSOL INC (CA)
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/organism="Homo sapiens"
/MD Lype="unassigned DNA"
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RESULT 7
AX008198
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Sequence 4 from Patent WO9967360. AX008198 AX008198.1 GI:9995823

linear DNA

181 GTGTGTTTCTGGAAGGAGCGAGCGCTGGGGTGGGCCCGGGCAACTACAGCTTCTCC 24	0y 481 CACCTAGTGTTGCGCTGGCTCCCCCCCCTGAGACACCTCACATCCCTACA 540 1	181	CGATGCAGGCAGGCGGGGACAGATGATGAGGGCCCCCTGCTGGAGCCAGTGGGCC 108 GTGAGCATGCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCG 114 GTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCG 114 GTGAGCATGCCCAGGATACCTATCTGGTGTGGACAAATGGTTGCTGCCCCGGAACCCG 114 GCAGTGAGGACCTCCCAGGGCCTGGTGGACAAATGGTTGCTGCCATGGATGAAGGC 120 CCAGTGAGGACCTCCCTGGTGGTGGAGTGTGGACATAGATGGCCATGGATGAAGGC 120 CAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCCAGGGGAGCCTCT 126 CAGAAGCATCCTCCTGCTCTTTGGCCTCGAAGCCCAGGGGAGCCTCT 126 CAGAAGCATCCTCCTGCTCTTTGGCCTCGAAGCCCAGGGGAGCCTCT 126 CAGAAGCATCCTCCTGCTCTTTGGCCTCGAAGCCCAGGGGAGCCTCT 126
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QY 601 GGCCGCACCGAGTGTGTGCTGAGCAACCTGCGGGGCCGGACGCGCTACACCTTCGCCGTC 660 LINE		781 GTCATCCTGGTGCTGACCGTGCTCGCGCTGCTCTCCCACCGCCGGGCTCTGAAGCAG	OY 841 AAGATCTGGCCTGGCATCCCGAGCGAGTTTGAAGGCCTCTTCACCACC 900	OY 901 AAGGTAACTICCAGCTGTAGCTGTACCAGAATGATGGCTGCCTGTGGTGGAGCCCCTGC 960	Oy 961 ACCCCTTCACGGAGGACCCACTGCTTCCCTGGAAGTCCTCTCAGAGGG 1020	1021 ACGATGCAGCGGTGGAGCCGGGGACAGATGATGAGGGCCCCTGCTGGAGCCAGTGGGC 1021 ACGATGCAGGCAGTGGGACAGATGATGATGAGGCCCCCTGCTGGAGCCAGTGGGG	1081 AGTGAGGATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCG 1081 AGTGAGCATGCCCAGGATACCTATCTGGTGCTGGACAAATGGTTGCTGCCCCGGAACCCG	1141 CCCAGTGAGGACCTCCCAGGGCCTGGTGGCAGTGTGGACATAGTGGCCATGGATGAAGGC	1201 TCAGAAGCATCCTCCTGCTCATCTGCTTTGGCCTCGAAGCCGAGCCGGAGGGAG	Oy 1261 GTGCCAGCTTTGAGTAACTGGACCCCAGCTCCAGCTTTGCCTTTGGT 1317 Db 1261 GCTGCCAGCTTTGAGTACACTATCCTGGACCCCAGCTCCCAGCTCTTGCGTCCATAG 1317	RESULT 10 BC019092 LOCUS BC019092 LOCUS BC019092 DEDITION DATA OF STANDISH OF	INAGE 4994283), partial cds. BC019092 BC019092.2 GI:40226074	SM Hom Buk	REFERENCE 1 (bases 1 to 2154) AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D., Alterhul, S.F., Zecherg, R. Hinstow, K. H., Schaefer, C.F., Bhat, N. K.	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soaree, M.B., Bonaldo, M.F., Casavant, T.L., Scheer, T.F., Rrownstein, M.J., Usdin, T.B., Toshivuki, S.,	Carning, Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Qy 1261 GCTGCCAGCTTTGAGTACACTATCCTGGACCCCAGCTCCCAGGTCTTGCGTCCATGG 1317	RESULT 9 AX008201 1317 bp DNA linear PAT 06-SEP-2000 LOCUS DEFINITION Sequence 7 from Patent W09967360. ACCESSION AX008201 GR 19995825 KEXRON AX008201.1 GI:9995825	, i	ARTHORS Matthews K.E., Bell, D. and Mueller, S.G. TITLE The efficient culture of stem cells for the production of hemoglobin	JOURNAL FACENT: WO 95/580-A / 29-DEC-1999; FEATURES Location/Qualifiers 1.1317 Source 1.1317	/mol type="unassigned DNA" /mol type="unassigned DNA" /db_xref="taxon:9606" ORIGIN	Ouery Match 85.6%; Score 1307.4; DB 6; Length 1317; Best Local Similarity 99.5%; Pred. No. 4.4e-219; Matches 1311; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	rccrragcccae rccrragcccaa	Qy 61 GGGGCCGCCTGGGCCCCCGCCTAACCTCCCGGACCCAAGTTCGAGGCAAAGCGGCC 120 Db 61 GGGGCCCCTGGGCGCCCCCGGCCCTAACCTCCCGGACCCCAAGTTCGAGGAAAGCGGCC 120	Oy 121 TTGCTGGCGGCCCGGAGGGCCCGAAGAGCTTCTGTGCTTCACCGAGGGTTGGAGGACGTTTG 180 Db 121 TTGCTGGCGGCCCGGAGGGCCCGAAGAGCTTCTGTGCTTCACCGAGGGGTTGGAGGACTTG 180	OY 181 GTGTGTTTCTGGGAGGAGGGGGGGGGGGGGCCGGGCAACTACAGCTTCTCC 240	Qy 241 TACCAGETCGAGGATGAGCCATGGAAGCTGTGTCGCCTGCACCAGGCTCCCACGGCTCGT 300 bb 241 TACCAGGTTCGAGGATGAGCATGGAAGCTGTGGCCTGCACGCTCCCACGGCTCGT 300	Oy 301 GGTGCGGTGCGCTTCTGGTGTTCGCTGCCTACAGCCGACACGTCGAGCTTCGTGCCCCTA 360 Db 301 GGTGCCGTACGGTGTTCGGTGTTCGCTACAGCCGACACGTCGAGCTTCGTGCCCTA 360	OY 361 GAGTIGCGCGTCACAGCAGCTCCGGCGTTCACCGTGTCACCATCATCAAT 420 	Qy 421 GAAGTAGTGCTCCTAGACGCCCCGTGGGGCTTGGCTGGCT	Oy 481 CACGTAGTGTTGCGCTGCCTCCCCCCTGAGACACCCATGACGTCTCACATCCGCTAC 540	Qy 541 GAGGTGGACGTCTCGGCCGCAACGCGCAGGGAGCGTACAGAGGGTGGAGATCCTGGAG 600

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgrl.nih.gov/
Contact: nisc_mgc@nhgrl.nih.gov/
Shkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plates 39 Row: j Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557561.
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worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M. Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                            NIH-WGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:19387983.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.
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(Dages 1 to 5761)

Jikuya, H., Takano, J., Nomura, N., Kikuno, R., Nagase, T. and Ohara, O. Direct Submission
Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
Institute, Department of Human Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                      Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O. The nucleotide sequence of a long cDNA clone isolated from human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 8.2e-214;
0; Mismatches 4; Indels 0;
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/gene="FLJ00153"
/note="Start codon is not identified."</pre>
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mol_type="mana"
db_xref="taxon:9606"
clone="FLJ00153"
    /tissue_type="spleen"
    /dev_stage="adult"
    /note="vector:pBluescriptII SK pl
                                                                                                                             5761 bp mRNA Homo sapiens mRNA for FL000153 protein. AK074082
  CCAGCTATGTGGCTTGCTCTTAG 1912
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fis (full insert sequence)
Homo sapiens (human)
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/gene="FLJ00153"
<595. .2088
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Best Local Similarity 99.7%;
Matches 1279; Conservative C
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TTGCTGGCGCCCGGGGCCCGAAGAGCTTCTGTGCTTCACCGAGCGGTTGGAGGACTTG
                                                             GIGIGITITCIGGGAGGAAGCGGCGAGCGCTGGGGTGGGCCCCGGGCAACTACAGCTICICC
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                                                                                                                           TACCAGCTCGAGGATGAGCCATGGAAGCTGTGGCCCTGCACCAGGCTCCCACGGCTCGT
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/note="cytokine receptor"
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GHVVLRWLPPPGAPWASLIRYEVNISTENAAGGVQRVEILDGRTECVLSNLRGGTRYT
FWYRANARAPSFGGFWSANGSTSLLARSDLDFLITLISLLLLLLLLLALLALLSHR
RTLKOKIWPGIPSPEGBREGLFTTHKGNFQLWLYQTDGCLWWSPCTPPRADPPAPLEV
LSERCWGVTQAVEPAADDEGSLLEPVGSEHARDTYLVLDKWLLPRRPASEDDPQPGGD
LDMAAMDEASEASFCSSALALKRGPEGASAASFEYTILDPSSQLLRPRPAEDPPTP
PHIKXLYLVVVSDSGISTDYSSGGSGETGGGSSGSPYSNPYENSLVPAPEPSPPNYTC
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                1504
                                 ATGGCCCCTACTCCAACCCTTATGAGAACAGCCTTATCCCCAGCGCGCTGAGCCTCTGCCCC 4961
                                                                                                                                                                            AF274305 1843 bp mRNA linear MAM 08-MAY-2003
Sus scrofa erythropoietin receptor mRNA, complete cds.
AF274305
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1 (bases 1 to 1843)

Pearson, P.L., Smith, T.P.L., Sonstegard, T.S., Klemcke, H.G., Christenson, R.K. and Vallet, J.L.

Christenson, R.K. and Vallet, J.L.

in embryonic and fetal liver

Domest. Anim. Endocrinol. 19 (1), 25-38 (2000)
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Submitted (01-JUN-2000) Reproduction Unit, Roman L. Hruska, U.S.
Meat Animal Research Center, P.O. Box 166, Clay Center, NE 68933.
                ATGGCCCCTACTCCAACCCTTATGAGAACAGCCTTATCCCCAGCCGCTGAGCCTCTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 1843)
Pearson, P. L., Smith, T.P.L., Sonstegard, T.S., Klemcke, H.G.
Christenson, R.K. and Vallet, J.L.
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Pred. No. 1.6e-192;
0; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="liver"
/dev_stage="fetus"
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'organism="Sus scrofa"
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1 ATGGACCACCTCGGGGCGTCCCTCTGGCCCCAGGTCGGCTCCTTTGTCTCCTGCTCGCT 6 28 ATGGACAAACTCAGGGTGCCCCTCTGGCCTCGGTAGGCCCCCTTTGTTCTCCTACTTGCT 40 GGGCCCCTGGGCGCCCCTCTGGCCTCCGGGTAGGCCCCCTCTGTTCTCTTGTTGT 41 GGGCCCCTGGGCGCCCCTAACCTCCCGGACCCCAAGTTCGAGAGCAAAGCGGCC 41		445 GAAGTAGTGCTCCTGGACGCGCGGGCTGCTGGCGCCCGGCCAGAAGAGGGCAGC 504 481 CACGTAGTGCTCCTGGCTCCCCCCCCCTGAGACCCCTGACGCAGCAGACGCCCGCTAC 481 CACGTAGTGTTGCGCTGGCTCCCCCCCCCTGAGACACGCTCTCACATCCGCTAC 505 CACGTGGTGCTGCGCTGCCTACCTCTGGAGCATATGACCACCCCACATCCGATAT 564 541 GAGGTGGACGCTCGGCCGCAACGGCAGGAGCGTACAGAGGTGGAGATCCTGGAG 600	661 CGGGGGGTATGGCTGAGCCGAGCTTCTGGAGGCCTGGTGGAGCCTGGT 720	
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	OY 1498 CTGCCCCCAGCTATGGCTTGCTCTAG 1527 OY 1498 CTGCCCCCAGCTATGGGCTTGCTCTAG 1527 Db 1660 TCACCCCCGAACTATGTGACCTGCTCTATG 1689 RESULT 13 WUSERPR LOCUS DEFINITION Mouse erythropoietin receptor (BPO-R) mRNA linear ROD 12-JUN-1993 DEFINITION MOUSE erythropoietin receptor (BPO-R) mRNA, complete cds. VERSION J04843. GI:193090 KEYWORDS erythropoietin receptor; hematopoietic growth factor receptor;	tränsmembrane protein. Mus musculus (house mouse) Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murina E 1 (bases 1 to 1741) E D'Andrea, A.D., Lodish, H.F. and Wong, G.G. Expression cloning of the murine erythropoietin receptor Cell 57 (2), 277-285 (1989) E 89195238 D 2539263 Original source text: Mouse erythroleukemia cell line MEL s 745, cDNA to mRNA, clone 190.	PEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers 1. 1741 / Organism="Mus musculus" / mol type="mRNA" / do_xref="taxon:10090" CDS 28. 1551 / note="erythropoietin receptor precursor" / codon start=1 / protein id="AAA37571.1" / db_xref="G1:309219" / translation="MUSKRYPIWPRYGPLCLLLAGAAWAPSPSLPDFKFESKAALLAS	RECEDENCY TREASONNERS STRUCTURE CONTROLL OF THE

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/clone lib="NCI CGAP_Mam5"
/lab_host="DH10E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLRWILPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLLEGRTECVLSNLRGGTRYTFAV RARMAEPSSSGFWAMWSEPASLLTASDLDPLILITSLILVIISLLLYLASLLSHRRTL QQKTWYGIPSPESEPEGLFTTHKGNPOLMLLORDGCLWWSPGSSFPEDPPAHLEVLSE PROKYTYGAGDPGADDEALLEVUSS VGSEHAQDTYLLDKYLLPRTPCSBNLSGPGGSVDP VTMDBASETSSCPSDLASKERPEGTSPSSFEYTILDPSSQLLCPRALPPEPPHL KYLYLVVSDSGISTDYSSGGSQCVHGDSSDGPYSHPYENSLVPDSEPLHPGYVACS"
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GSEELLCFTQRLEDLVCFWEEAASSGMDFNYSFSYQLEGESRKSCSLHQAPTVRGSVR
FWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVLLDAPAGLLARRAEEGSHV
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                                                                                                                                                                                                       Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. (LLNL)
Lothary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943
Mttp://www.engc.stanford.edu
Contact: (Dickson, Mark) mcdepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 7 Row: 1 Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590
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/note="FN3; Region: Fibronectin type 3 domain"
/db_xref="CDD:cd00063"
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Pred. No. 4.9e-179;
0; Mismatches 269; Indels
                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/db_xref="taxon:10090"
/clone="IMAGE:3487672"
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/organism="Mus musculus"

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/product="Epor
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Best Local Similarity 82.2
Matches 1253; Conservative
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.E., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soares, M.M. B., Bonaldo, M.F., Casarant, T.L., Scheefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Munny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S. Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Dickson, M.C., Rodrigues, S., Chnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,                                                                                                                                                                                                                                                                                                                                            1260
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                                                     CTGTGCCCTGAGCTGCCCCCTACCCCACCCCAAAGTAACTTACCTGTACCTTGTGGTATCT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1465 TCTGATGGCCCCTACTCCCCCCCTATGAGAACAGCCTTGTCCCAGACTCAGAGCCTCTG 1524
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                             1225 TCAGAAACATCTTCCTGCCCGTCTGACTTGGCCTCAAAGCCCAGGCCAGAGGGGACCTCA
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgici.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakeeley,R.W., Ganite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon10090"
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/tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5
old mouse. Taken by biopsy."
/clone lib="NCI CGAP_Mam2"
/lab_host="DH10B"
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/note="FN3; Region: Fibronectin type 3 domain"
/db_xref="CDD:smart00060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Pred. No. 1.5e-178;
); Mismatches 272; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
1. .1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Epor"
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/db_xref="MGI:95408"
76. 1599
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/protein_id="AAH46282.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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82.0%;
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Matches 1252; Conserv
      Sequencing
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